

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 06:36:22 ; Search time 140 Seconds
(without alignments)
6342.296 Million cell updates/sec

Title: US-09-784-810C-1
Perfect score: 1600
Sequence: 1 nccccccggggtccctatag.....aaataagtgacattcccaa 1600

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/prodata/2/1na/5A_COMB.seq: *
2: /cgn2_6/prodata/2/1na/5B_COMB.seq: *
3: /cgn2_6/prodata/2/1na/6A_COMB.seq: *
4: /cgn2_6/prodata/2/1na/6B_COMB.seq: *
5: /cgn2_6/prodata/2/1na/PCITUS_COMB.seq: *
6: /cgn2_6/prodata/2/1na/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	ID	Description
1	1426.8	89.2	1533	4	US-09-205-258-90
2	1124.6	70.3	1155	4	US-09-970-516-1
3	742.4	46.4	1149	4	US-09-970-516-5
4	258	16.1	1857	4	US-09-970-516-3
5	49.6	3.1	1203	3	US-09-086-010-1
6	48.6	3.0	4403765	3	US-09-103-840A-2
7	47.8	3.0	900	5	PCT-US95-04801-3
8	47.2	3.0	2793	1	US-08-209-747-1
9	47.2	3.0	2793	1	US-08-458-298-1
10	47	2.9	68750	3	US-09-335-409-1
11	47	2.9	68750	4	US-09-568-102-1
12	47	2.9	68750	4	US-09-567-969-1
13	47	2.9	68750	4	US-09-568-480-1
14	47	2.9	68750	4	US-09-568-486-1
15	47	2.9	68750	4	US-09-568-472-1
16	47	2.9	68750	4	US-09-568-899-1
17	46.6	2.9	2011	6	5256770-6
18	46.4	2.9	993	4	US-09-252-991A-2002
19	46.4	2.9	1221	4	US-09-252-991A-2160
20	46.4	2.9	1269	4	US-09-252-991A-2089
21	46.4	2.9	1482	4	US-09-252-991A-1723
22	46.4	2.9	1506	4	US-09-252-991A-1875
23	46.4	2.9	53526	3	US-08-658-136-2
24	46.4	2.9	53577	3	US-08-658-136-1
25	45.2	2.8	918	4	US-09-252-991A-1131
26	45.2	2.8	1338	4	US-09-252-991A-1058
27	45	2.8	441529	3	US-09-103-840A-1

28	44.8	2.8	1164	1	US-07-640-476-6	Sequence 6, Appl
29	44.8	2.8	1614	4	US-09-616-289-45	Sequence 45, Appl
30	44.8	2.8	12425	4	US-09-616-289-50	Sequence 50, Appl
31	44.6	2.8	4257	2	US-08-690-473-1	Sequence 1, Appl
32	44.6	2.8	4257	3	US-08-259-821A-1	Sequence 1, Appl
33	44.6	2.8	4257	3	US-08-843-659-1	Sequence 1, Appl
34	44.6	2.8	12001	1	US-08-458-568A-11	Sequence 11, Appl
35	44.4	2.8	759	4	US-09-252-991A-1802	Sequence 1802, Ap
36	44.2	2.8	1119	4	US-09-252-991A-1375	Sequence 1375, A
37	44.2	2.8	2349	4	US-08-252-991A-1376	Sequence 1376, A
38	44.2	2.8	3081	4	US-08-252-991A-1360	Sequence 1360, A
39	44.2	2.8	4403765	3	US-09-103-840A-2	Sequence 2, Appl
40	43.8	2.7	71989	4	US-09-443-501A-2	Sequence 2, Appl
41	43.4	2.7	505	4	US-09-621-976-15639	Sequence 15639, A
42	43.4	2.7	1921	3	US-08-482-677-3	Sequence 3, Appl
43	43.4	2.7	1921	4	US-10-033-174-3	Sequence 3, Appl
44	43.4	2.7	1926	1	US-08-152-019A-43	Sequence 43, Appl
45	43.2	2.7	759	4	US-09-252-991A-9217	Sequence 9217, Ap

ALIGNMENTS

RESULT 1
US-09-205-258-90
Sequence 90, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06

Db 1147 CTTCTGATGATGAGGGTTGGCTGAGGCCCGCCAGCTGGAAGCCCGAGATGCC 1206
QY 1309 ACCGCGAGAGAGCCCTTATGACCCCTGGCGCGCTGTGCTTATGTTACTTGACG 1358
Db 1207 ACCGCGAGAGAGCCCTTATGACCCCTGGCGCGCTGTGCTTATGTTACTTGACG 1266
QY 1369 ACCCTTCCCTTCCCTTATGAGGCTGAGGCGCTGTGCTTATGTTACTTGACG 1428
Db 1267 ACCCTTCCCTTCCCTTATGAGGCTGAGGCGCTGTGCTTATGTTACTTGACG 1326
QY 1429 ACTCTCTGAGAGAGGCTGAGAGGCTGAGGCTTATGTTACTTGACG 1488
Db 1387 ACTCTCTGAGAGAGGCTGAGAGGCTGAGGCTTATGTTACTTGACG 1386
QY 1489 AGTCTGGGTGAGAGCCAGCTGAGGCGCTGAGGCTTATGTTACTTGACG 1548
Db 1387 AGTCTGGGTGAGAGCCAGCTGAGGCGCTGAGGCTTATGTTACTTGACG 1446
QY 1549 GTTCTGAGAGCCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1600
Db 1447 GTTCTGAGAGCCCGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1498

RESULT 2

US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 1155
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-09-970-516-1

Query Match 70.3%; Score 1124.6; DB 4; Length 1155;
Best Local Similarity 98.4%; Pred. No. 1.6e-248;
Matches 1136; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 176 ATGATTCAGCGGCG 235
Db 1 ATGATTCAGCGGCG 60
QY 236 CTGAACCG 295
Db 61 CTGAACCG 120
QY 236 CTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGCGCGGAGCCAG 355
Db 121 CTTTGGCTGAGGCTGAATCTCTTCAAGCTGATGCTCACTGAGCGCGGAGCCAG 180
QY 356 CGGAGAGCTGAGGCTGAGGAGAGCTGAGGAGCGCTGAGGAGCGCTGAGGAGCG 415
Db 181 CGGAGAGCTGAGGCTGAGGAGAGCTGAGGAGCGCTGAGGAGCGCTGAGGAGCG 240
QY 416 GACGGGCTGATGCAAGAGTGTGAGACGGGCTCATGAGCGGCGCTGAGGAGCGCC 475
Db 241 GACGGGCTGATGCAAGAGTGTGAGACGGGCTCATGAGCGGCGCTGAGGAGCGCC 300
QY 476 ATCCGAAGAGCCCTGTGAGCTCCAGAGAGCTCTGGCAACGGCTGGCAAGCTTCTG 535
Db 301 ATCCGAAGAGCCCTGTGAGCTCCAGAGAGCTCTGGCAACGGCTGGCAAGCTTCTG 360

QY 536 AACCATTAAGCTGGCTATGAGAGGCTCACCAATGAAGAGCTCTCTGACCACTGACAGCTA 595
Db 361 AACCATTAAGCTGGCTATGAGAGGCTCACCAATGAAGAGCTCTCTGACCACTGACAGCTA 420
QY 596 TTGCTGAGCGCGCGGCTGCTGATGACCAATGAAGCTGCTGCTGACAGCGCTTGGGG 655
Db 421 TTGCTGAGCGCGCGGCTGCTGATGACCAATGAAGCTGCTGCTGACAGCGCTTGGGG 480
QY 656 CTGCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
Db 481 CTGCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 716 AGTATTAAGATGAGGAGCTGAGGAGAGATGAGGAGCTTCACTGCTGAGGAGCTTCTG 775
Db 541 AGTATTAAGATGAGGAGCTGAGGAGAGATGAGGAGCTTCACTGCTGAGGAGCTTCTG 600
QY 776 GCAAGCTGAGCACTTACCGCGCGAGCTGAGCTTCACTGCTGAGGAGAGTGGCTTTC 835
Db 601 GCAAGCTGAGCACTTACCGCGCGAGCTGAGCTTCACTGCTGAGGAGAGTGGCTTTC 660
QY 836 AAGACACTGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
Db 661 AAGACACTGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 896 CTGAGAGAGAGGCTGCTTCTCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
Db 721 CTGAGAGAGAGGCTGCTTCTCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 956 CTGAGAGAGGCTGCTTCTCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
Db 781 CTGAGAGAGGCTGCTTCTCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 1016 GCAAGCTGAGCACTTACCGCGCGAGCTGAGCTTCACTGCTGAGGAGCTTCTG 1075
Db 841 GCAAGCTGAGCACTTACCGCGCGAGCTGAGCTTCACTGCTGAGGAGCTTCTG 960
QY 1076 CGCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
Db 901 CGCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 1136 TATGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1195
Db 961 TATGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1196 GATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1255
Db 1021 GATGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1256 ATGCTCAGCGGCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1315
Db 1081 ATGCTCAGCGGCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1316 GAAGAGCCCTTATGA 1330
Db 1141 GAAGAGCCCTTATGA 1155

RESULT 3

US-09-970-516-5
; Sequence 5, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 5
; LENGTH: 1149

Db 768 TGAAGCAGCCCTGGGCTTGACCTGTGTCTCACTGCTCACTGTGTCTGTGTGCGGAGTGG 827
Qy 613 GGTGTACCCATGAACCTGTGTCTCTGTGACACGGCTTGGGGCTGCGCTGTCTGTGT 672
Db 828 TGGACACCCACTGAGCTGTGTCTGTGTGACGCTGCGCTTGGGGCTGCGCTGTCTGTGT 887
Qy 673 GGTGACCCCTGGGCTTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 732
Db 888 CTTGT 947
Qy 733 TGTGGGAGATGCGCTTGT 792
Db 948 CTTGGGAGATGCGCTTGT 1007
Qy 793 CCGGGGCGACTGT 818
Db 1008 CCGGGGCGACTGT 1033

RESULT 5

US-09-086-010-1
Sequence 1, Application US/09086010
Patent No. 6274338
GENERAL INFORMATION:
APPLICANT: Glimcher, Laurie H. et al.
TITLE OF INVENTION: Human c-Maf Compositions and
METHOD OF INVENTION: Methods of Use Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,010
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/030,579
FILING DATE: 2-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: HUT-027CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)227-7400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1203
US-09-086-010-1

Query Match 3.1%; Score 49.6; DB 3; Length 1203;
Best Local Similarity 45.6%; Pred. No. 0.023;
Matches 15; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
Qy 3 CCCCCGGGGTCTTATAGCCACGCTCCGAGGGGAGGCGAGGCCACAGCCGGCCCT 62
Db 494 CCGCGGTGATCG 553

Qy 63 GCGACGCCCTCTGGGAGACCGGATAGAGCTGAAGGAGAGAGCCGCCCAAGGCA 122
Db 554 ACCACACAGCGCGCGCGCGCACACACACCGAGCGCGCGCGCGCGCGCGCGCA 613
Qy 123 GCGGCCCCACAGCGCGCGAGACCCCTGTGAGCGAGAGCGCGCGGATGATGATG 182
Db 614 GCGGCGCGCTTGTGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 673
Qy 183 CAGCGGCG 242
Db 674 GCGGCG 733
Qy 243 CCG 302
Db 734 CCGACACG 793
Qy 303 CTGAGGCTGAATCTCTTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362
Db 794 CCATGTCTGTGCGGACTGTGAACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 853
Qy 363 TGTGCGGTGCGAGGAGCTTGGCC 386
Db 854 GCGTGAAGCAAGAGCGGAGCC 877

RESULT 6

US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 3.0%; Score 48.6; DB 3; Length 4403765;
Best Local Similarity 47.2%; Pred. No. 0.32;
Matches 179; Conservative 0; Mismatches 199; Indels 1; Gaps 1;

Qy 3 CCCCCGGGGTCTTATAGCCACGCTCCGAGGGGAGGCGAGGCCACAGCCGGCCCT 62
Db 3942920 CCGCGGAGGCTCCAGTCTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 3942861
Qy 63 GCGACGCCCTCTGGGAGACCGGATAGAGCTGAAGGAGAGCGCGCGCGCGCGCGCA 122
Db 3942860 CCGCGGTACCAACCGTTTACACCGTTTACACCGTGTGTGTGTGTGTGTGTGT 3942801
Qy 123 GCGCC-CCCAAGGCGCAAGGACCCCTGTGAGCGGAGCGCGCGGTGTGAGTTAGAT 181
Db 3942800 GCGCGTCTGT 3942741
Qy 182 CCAAGCGGCG 241
Db 3942740 CTGCGGT 3942681
Qy 242 CCGCGCGCGCGCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301

Db 3942680 CCGCCGTTGCGCCGCGGCTGCGGCTGAGCTTACCCCGCCGCTACCGCGCGCCCGCCG 3942621
QY 302 GCTGAGGCTGAAATCTCTTACGCTGATGCTCACTGAGCGCGGACCAACGCGCGGAG 361
Db 3942620 CTGCGCGCGGCTGCGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTG 3942561
QY 362 CTGCTGCGCTGCGAGGAGC 380
Db 3942560 CTTGCGTTGCGCGCGCTGCG 3942542

RESULT 7

PCT-US95-04801-3
Sequence 3 Application PC/TUS9504801
GENERAL INFORMATION:
APPLICANT: Martin, Juan F.
APPLICANT: Coque, Juan R.
APPLICANT: Enguita, Francisco J.
APPLICANT: Fuente, Juan L.
APPLICANT: Llaena, Francisco J.
APPLICANT: Liras, Paloma
TITLE OF INVENTION: DNA ENCODING CEPHARANTIN BIOSYNTHESIS
TITLE OF INVENTION: LATE GENES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-04801-3

Query Match 3.0%; Score 47.8; DB 5; Length 900;
Best Local Similarity 51.1%; Pred. No. 0.054;
Matches 112; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 185 GCGGCGGCG 244
Db 353 GCGGCG 412
QY 245 GCGGCG 304
Db 413 GCGGCG 472
QY 305 GAGGCTGAATCTCTTCAAGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 364
Db 473 CAGATCAATCAAGCTGCTGCTG 532

QY 365 GTGCGGTGAGAGAGCTGCGCGCGCTGAGAGCTCTGAGT 403
Db 533 TGCAGCTACCGGTGCTGAGACTGTCCGCCGACTGAGT 571

RESULT 8

US-08-209-747-1
Sequence 1 Application US/08209747
Patent No. 5733771
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding Minor Ampullate Spider
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DATE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
FEATURE:
NAME/KEY: CDS
LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
US-08-209-747-1

Query Match 3.0%; Score 47.2; DB 1; Length 2793;
Best Local Similarity 47.1%; Pred. No. 0.1; Indels 163; Gaps 0;
Matches 145; Conservative 0; Mismatches 163;

QY 151 GCAGCGGAGCGCGCGGTGAGTATGATCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 210
Db 1331 GCAGAGCGCGGTGCGCGGTGAGAGCTGAGAGCTACGATGATGATGATGATGATGATGATGATG 1390
QY 211 GCGGCG 270
Db 1391 GGTGAGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1450
QY 271 GCTCTTCGAGAGTCAAGTCAAGCG 330
Db 1451 GGTAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1510
QY 331 GCTACTGAGCGCGGAAACACGCGCGGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

QY 20 GCCACGCTCCCGGCGGGAGGCGAGCCCGACAGCCGCGCTGCG-ACGCCGCGCTGGG 78
DB 56200 GCCGTGCGCGCGGCGGCGGACCGCGCTTCGCGGGGCTGAGCGCGCTTCAGCGG 56259
QY 79 CAGCACCAGTAAGAGACTGAAGGCAAGAGCCCGCGCAGGCGGCGCCCGACAGCGCC 138
DB 56260 CACCAACGTCCAGTGTCTGAGAGGCGCGCGCGCGCTGCGACCGCGCGAGCGCC 56319
QY 139 AGGAGCCCGCTGCGAGCGGAGCGCGGCTGAGTTATGATCCAGCGCGCGCGCGCG 198
DB 56320 GGGGCGCTCAGCGGAGCTTTTGTGCTGTCGCGGAAGAGCGCGCGCTGGAAGCA 56379
QY 199 GGGCGTCTCCGCGGCGCTGCGCGCTGCTGCTGCTGCTGAACCGCGCGCGCGAGGG 258
DB 56380 GGGGCGCGCGCTCTCAGCGCACATCCCGCTACCGCGAGCGAGGCTTCGAGAGCTGCG 56439
QY 259 CAGGCGCTTGCAGCTCTTCCGAGTCAAGTCAAGCCCGCTTTTGGCTGAGAGTGAATCTC 318
DB 56440 GTTCAGCTGTGATTCAGACCGGTAACCGCATGAGACACCGCTGCGGTGCGGAGCTTC 56499
QY 319 CTTACGCTGATGCTCACTGAGCGCGGAGCAACCGCGCGGAGCTGTGCGAGGA 378
DB 56500 GCGCGAGCGCTGCGGAGCGCGCTGAGGTTGCGGCGAGGCGAGACCGCGCGAGCGCG 56559
QY 379 GCTGGCGCGCTGGAGCGCT 397
DB 56560 GCGCGCGCGAGGCGCGCT 56578

RESULT 14
US-09-568-486-1
; Sequence 1, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-486-1

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

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; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 68750
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-472-1

Query Match 2.9%; Score 47; DB 4; Length 68750;
Best Local Similarity 47.0%; Pred. No. 0.26;
Matches 178; Conservative 0; Mismatches 200; Indels 1; Gaps 1;

QY 20 GCCACGCTCCCGGCGGGAGGCGAGCCCGACAGCGCGCGCTGCG-ACGCCGCGCTGGG 78
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Mon Mar 1 09:38:57 2004

us-09-784-810c-1.rml

Page 10

Db 56560 GCGCGCGCGAGGCGCT 56578

Search completed: February 27, 2004, 09:46:05
Job time : 155 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2004, 09:46:12 ; Search time 569 Seconds

(without alignments)
10144,019 Million cell updates/sec

Title: US-09-784-810C-1

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Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 180373377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1426.8	89.2	1533	US-09-933-767-80	Sequence 9, Appl
4	1426.8	89.2	1533	US-10-023-282-90	Sequence 90, Appl
5	1387.2	86.7	1562	US-10-264-237-1180	Sequence 1180, Ap
6	1124.6	70.3	1155	US-09-970-516-1	Sequence 1, Appl
7	1120	70.0	1152	US-10-348-052-22	Sequence 22, Appl
8	836.4	52.3	1759	US-09-784-810A-3	Sequence 3, Appl
9	742.4	46.4	1149	US-09-970-516-5	Sequence 5, Appl
10	382.6	23.9	394	US-09-954-456-1756	Sequence 1756, Ap
11	286.6	17.9	480	US-09-783-590-9248	Sequence 9248, Ap
12	258	16.1	1857	US-09-970-516-3	Sequence 3, Appl
13	258	16.1	2380	US-09-817-676A-13	Sequence 13, Appl
14	258	16.1	2380	US-10-354-358-77	Sequence 77, Appl
15	242	15.1	2698	US-09-817-676A-11	Sequence 11, Appl

16	197.4	12.3	199	US-09-796-692-2905	Sequence 2905, Ap
17	197.4	12.3	199	US-10-040-862-2905	Sequence 2905, Ap
18	197.4	12.3	199	US-10-057-475B-2905	Sequence 2905, Ap
19	197.4	12.3	199	US-10-154-884B-2905	Sequence 2905, Ap
20	193	12.1	296	US-09-777-564-658	Sequence 658, App
21	193	12.1	296	US-10-015-219-658	Sequence 658, App
22	176.8	11.1	585	US-10-027-637-196470	Sequence 196470, A
23	117.8	7.4	428	US-10-191-803-456	Sequence 456, App
24	114.4	7.2	832	US-10-029-386-20952	Sequence 20952, A
25	114.4	7.2	1394	US-10-264-049-204	Sequence 204, App
26	102	6.4	507	US-10-029-386-7252	Sequence 7252, Ap
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29	83.4	5.2	2639	US-10-348-052-24	Sequence 24, Appl
30	64.6	4.0	2084	US-10-424-599-43396	Sequence 43396, A
31	60	3.8	60	US-09-908-975-14378	Sequence 14378, A
32	53.8	3.4	732	US-10-259-165-115	Sequence 115, App
33	52	3.2	7185	US-10-329-079-48	Sequence 25926, A
34	52	3.2	61944	US-10-329-079-34	Sequence 48, Appl
35	52	3.2	2136	US-10-156-761-7476	Sequence 7476, Ap
36	51.8	3.2	3135	US-10-156-761-5936	Sequence 5936, Ap
37	51.8	3.2	51657	US-10-057-475B-10475	Sequence 10475, A
38	51.8	3.2	51657	US-10-154-884B-10475	Sequence 10475, A
39	51.8	3.2	9025608	US-10-156-761-1	Sequence 1, Appl
40	51.8	3.2	9025608	US-10-156-761-1	Sequence 1, Appl
41	51.8	3.2	1614	US-09-969-896-15	Sequence 15, Appl
42	51.2	3.2	4413	US-10-120-988-148	Sequence 148, App
43	51.2	3.2	4413	US-10-315-597A-1	Sequence 1, Appl
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ALIGNMENTS

RESULT 1
US-09-784-810A-1
Sequence 1, Application US/09784810A
Patent No. US20020082203A1
GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 10746-08
CURRENT APPLICATION NUMBER: US/09/784, 810A
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1600
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: a, t, c, g, other or unknown
US-09-784-810A-1

Query Match 99.9%; Score 1599; DB 9; Length 1600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; PRIOR APPLICATION NUMBER: 60/048,885

;; PRIOR APPLICATION NUMBER: 60/048,885

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QY	290	CAGCCCCCTTTGGCT	GAGGCTGAATCTCT			
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; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; CURRENT FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
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EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
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LENGTH: 1533
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (1527)
OTHER INFORMATION: n equals a,t,g, or c
US-10-023-282-90

Query Match 89.2%; Score 1426.8; DB 14; Length 1533;
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Matches 1459; Conservative 6; Mismatches 25; Indels 2; Gaps 2;
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DB 8 GCCGNCACGGGAGCG-CCCATAGCGCAGGACCCCTGGCAGCGGAGCGCGGTC 66
QY 170 GAGTTATGATCCAGCGCGCGCCCGCGCGTGTCTCCGCGGCCCTGCGCGTGTG 229
DB 67 GAGTTATGATCCAGCGCGCGCCCGCGCGTGTCTCCGCGGCCCTGCCGTTGCTG 126
QY 230 GTGCTGCTGAACCGCGCGCGCAGGGCAAGCCCTTCGAGCTCTTCGGAGTACGTG 289
DB 127 GTGCTGCTGAACCGCGCGCGCAGGGCAAGCCCTTCGAGCTCTTCGGAGTACGTG 186
QY 290 CAGCCCCCTTTGCTGAGGTGAAATCTCTTCACTGATGTCTCACTGAGCGGCGAAC 349
DB 187 CAGCCCCCTTTGCTGAGGTGAAATCTCTTCACTGATGTCTCACTGAGCGGCGAAC 246
QY 350 CAGCGCGGAGTGTGCGGTTCGAGGAGCTGGCGCGCTGGGACGCTCTGTTGTCATG 409
DB 247 CAGCGCGGAGTGTGCGGTTCGAGGAGCTGGCGCGCTGGGACGCTCTGTTGTCATG 306

QY 410 TCTGGAGACGGGCTGATGCACGAGGTGTGAACGGG-TCATGGAGCGGCTGACTGGGA 468
DB 307 TTTGGAGACGGGCTGATGCACGAGGTGTGAACGGGTTTCATGGAGCGGCTGACTGGGA 366
QY 469 GACCGCCATCCAGAAGCCCTGTGTAGCCTCCAGCAGGCTCTGGCAACCGGTGGCAGC 528
DB 367 GACCGCCATCCAGAAGCCCTGTGTAGCCTCCAGCAGGCTCTGGCAACCGGTGGCAGC 426
QY 529 TTTCTTGAACCATTAATGCTGGCTATGAGCAGGTGACCAATGAAGACCTCTCTGACCACTG 588
DB 427 TTTCTTGAACCATTAATGCTGGCTATGAGCAGGTGACCAATGAAGACCTCTCTGACCACTG 486
QY 589 CACGCTATTGCTGTCCCGCCCGGTGTGTCAACCATGAACCTGTGTCTGTGACACGGC 648
DB 487 CACGCTATTGCTGTCCCGCCCGGTGTGTCAACCATGAACCTGTGTCTGTGACACGGC 546
QY 649 TTTGGGGTGGCTGCTTCTCTGTGTCTGAGCTGGCTGGGCTTCATTTGCTGATGGA 708
DB 547 TTTGGGGTGGCTGCTTCTCTGTGTCTGAGCTGGCTGGGCTTCATTTGCTGATGGA 606
QY 709 CCTAGAGAGTATAAGTATCGGCTCTGGGGGAGATGCGCTTCACTCTGGGCACTTCCT 768
DB 607 CCTAGAGAGTATAAGTATCGGCTCTGGGGGAGATGCGCTTCACTCTGGGCACTTCCT 666
QY 769 GCGTCTGGCAGCCCTGCGACCTACCGCGCGCAGCTGGCTACCTCCCTGTAGGAAAGT 828
DB 667 GCGTCTGGCAGCCCTGCGACCTACCGCGCGCAGCTGGCTACCTCCCTGTAGGAAAGT 726
QY 829 GGGTTTCAAGACACCTGCTTCCCGCTGTGTTCAGCAGGCGCCCGGTAGATGCACACT 888
DB 727 GGGTTTCAAGACACCTGCTTCCCGCTGTGTTCAGCAGGCGCCCGGTAGATGCACACT 786
QY 889 GGTGCCACTGGAGAGCAGTGTCTTCTCACTGGCAGTGGTGTCCCGCAGGACTTTGT 948
DB 787 TGTGCCACTGGAGAGCAGTGTCTTCTCACTGGCAGTGGTGTCCCGCAGGACTTTGT 846
QY 949 GCTAGTCTGCACTGCTGCACCTGGCAGTGGCAGTGGTGTTCGCTCACCCTATGG 1008
DB 847 GCTAGTCTGCACTGCTGCACCTGGCAGTGGCAGTGGTGTTCGCTCACCCTATGG 906
QY 1009 CCGCTGTGCAGTGGCTCATGCTTCTTCTAGTGGGCGGGAGTGTCTCTGTGCCAT 1068
DB 907 CCGCTGTGCAGTGGCTCATGCTTCTTCTAGTGGGCGGGAGTGTCTCTGTGCCAT 966
QY 1069 GCTGCTGGCTCTTCTTGGCAGTGGAGAGGGGAGGCAATGAGATGATGAATGCCCTA 1128
DB 967 GCTGCTGGCTCTTCTTGGCAGTGGAGAGGGGAGGCAATGAGATGATGAATGCCCTA 1026
QY 1129 CTTGCTATATGTGCCCTGTGTGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTGTGTT 1188
DB 1027 CTTGCTATATGTGCCCTGTGTGCTTCCGCTTGGAGCCCAAGGATGGGAAAGTGTGTT 1086
QY 1189 TGCAGTGGATGGGAAATTGATGTTAGCGAGCGCTGCGAGGCGAGGTGCACCCAACTA 1248
DB 1087 TGCAGTGGATGGGAAATTGATGTTAGCGAGCGCTGCGAGGCGAGGTGCACCCAACTA 1146
QY 1249 CTTTGTGATGTGTGAGCGTTCGCTGGAGCCCGCCAGCTGGAAGCCCGCAGCAGATGCC 1308
DB 1147 CTTTGTGATGTGTGAGCGTTCGCTGGAGCCCGCCAGCTGGAAGCCCGCAGCAGATGCC 1206
QY 1309 ACCGCCAAGAGCCCTTATGACCCCTGGGCGCGCTGTGCTTGTCTTACTTGCAGG 1368
DB 1207 ACCGCCAAGAGCCCTTATGACCCCTGGGCGCGCTGTGCTTGTCTTACTTGCAGG 1266
QY 1369 ACCCTTCTCTTCTTGGCTGAGGCTGTGCAAGCTCTGTGGGCTGTGGGCTGTGGAG 1428
DB 1267 ACCCTTCTCTTCTTGGCTGAGGCTGTGCAAGCTCTGTGGGCTGTGGGCTGTGGAG 1326
QY 1429 ACTCTCTGGAAGAGGCTGGAAGTGAAGCTATGCTTTGGGGGGGACAGGCCAAGATGA 1488
DB 1327 ACTCTCTGGAAGAGGCTGGAAGTGAAGCTATGCTTTGGGGGGGACAGGCCAAGATGA 1386
QY 1489 AGTCTGTGGTTCAGGAGCCCGAGCTGGCTGGGCGCCAGCTGGCTATGTAAGGCCCTTCTAGTTT 1548

1387 AGTCTGGGTGAGGAGCCAGCTGCTGGGCCAGCTGCTCTATGTAAGGCTTCTAGTTT 1446
1549 GTTCTGAGACCCCAACCCCAAGAAACCAATCCAAATAAAGTGACATTCCTCAA 1600
1447 GTTCTGAGACCCCAACCCCAAGAAACCAATCCAAATAAAGTGACATTCCTCAA 1498

RESULT 5

US-10-264-237-1180/c
Sequence 1180, Application US/10264237
Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA3131PI
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1180
LENGTH: 1562
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (12)..(12)
OTHER INFORMATION: n equals a,t,g, or c
S-10-264-237-1180

Query Match 86.7%; Score 1387.2; DB 15; Length 1562;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1398; Conservative 1; Mismatches 19; Indels 0; Gaps 0;
Y 193 CAGCGGGCGGCCCCCGGGCGTGTCTCCCGCGCCCTGCGCGTCTGCTGCTGCTGAACC 242
b 1455 CAGCGGGCGGCCCCCGGGCGTGTCTCCCGCGCCCTGCGCGTCTGCTGCTGAACC 1396
Y 243 CCGCGGGCGGCAAGGCAAGGCGCTTGACGCTCTCCGAGTCACGTGCGAGCCCTTTTGG 302
b 1395 CGCGGGCGGCAAGGCAAGGCGCTTGACGCTCTCCGAGTCACGTGCGAGCCCTTTTGG 1336
Y 303 CTGAGGCTGAAATCTCTTCACGCTGATGCTACGTAGCGCGGGAACCAACGCGGGAGC 362
b 1335 CTGAGGCTGAAATCTCTTCACGCTGATGCTCACTGAGCGGCGGAACCAACGCGGGAGC 1276
Y 363 TGGTCGGGTGCGAGAGCTGGGCGCTGGGAGCTCTGGTGTCTGCTGCTGAGACCGGC 422
b 1275 TGGTCGGGTGCGAGAGCTGGGCGCTGGGAGCTCTGGTGTCTGCTGCTGAGACCGGC 1216
Y 423 TGATGACAGAGTGTGTGAACGGGCTCATGGAGCGGCGCTGCTGAGAGACCGCCATCCAGA 482
b 1215 TGATGACAGAGTGTGTGAACGGGCTCATGGAGCGGCGCTGCTGAGAGACCGCCATCCAGA 1156
Y 483 AGCCCTGTGTAGCTTCCAGAGGCTCTGCAAGCGGCTGGAGCTTCTTGAACCAT 542
b 1155 AGCCCTGTGTAGCTTCCAGAGGCTCTGCAAGCGGCTGGAGCTTCTTGAACCAT 1096
Y 543 ATGCTGGCTATGACAGGCTCAACCAATGAACCTCTGACCAACGTGACGCTATTGCTGT 602
b 1095 ATGCTGGCTATGACAGGCTCAACCAATGAACCTCTGACCAACGTGACGCTATTGCTGT 1036
Y 603 GCCGCCCGGTGCTGTACCCATGAACCTGCTGTCTGTGCAACCGGCTGGGGGTGGCT 662
b 1035 GCCGCCCGGTGCTGTACCCATGAACCTGCTGTCTGTGCAACCGGCTGGGGGTGGGCC 976

QY 663 CGTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCAATTGCTGATGTGGACCTAGAGAGTGATA 722
Db 975 TCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCAATTGCTGATGTGGACCTAGAGAGTGAGA 916
QY 723 AGTATCGGCGCTCTGGGGAGATGCGCTTCACTCTGGGACACCTTCTCTGCGTCTGCGACGCC 782
Db 915 AGTATCGGCGCTCTGGGGAGATGCGCTTCACTCTGGGACACCTTCTCTGCGTCTGCGACGCC 856
QY 783 TGGCACCTTACCGCGCGCAGCTGGCTACCTCCCTGTAGGAAGAGTGGGTTTCAAGACAC 842
Db 855 TGGCGCACCTTACCGCGCGCAGCTGGCTACCTCCCTGTAGGAAGAGTGGGTTTCAAGACAC 796
QY 843 CTGCTTCCCGCTGTGGTCCAGCAGGCGCGGTAGATGCACACCTGGTGGCCTGAGG 902
Db 795 CTGCTTCCCGCTGTGGTCCAGCAGGCGCGGTAGATGCACACCTGGTGGCCTGAGG 736
QY 903 AGCAGTGTCTTCTCACTGGCAGGTGGTCCCGACGAGGACTTTGTGTAGTCTCTGCGAC 962
Db 735 AGCCAGTGTCTTCTCACTGGCAGGTGGTCCCGACGAGGACTTTGTGTAGTCTCTGCGAC 676
QY 963 TGGTGCACCTGGCAGCTGGCAGGTGGTGGTGTGCTGCACCCATGGCGCGCTGTCAGCTG 1022
Db 675 TGGTGCACCTGGCAGCTGGCAGGTGGTGGTGTGCTGCACCCATGGCGCGCTGTCAGCTG 616
QY 1023 GCGTCATGCACTGTGTTTCTACGTGCGGGCGGGAGTGTCTGTCGCACTGCTGCTCGCTCT 1082
Db 615 GCGTCATGCACTGTGTTTCTACGTGCGGGCGGGAGTGTCTGTCGCACTGCTGCTCGCTCT 556
QY 1083 TCTGCGCATGGAGAAAGGCGAGCATATGAGATGATGAATGCCCTACTTGGTATATGTGC 1142
Db 555 TCTGCGCATGGAGAAAGGCGAGCATATGAGATGATGAATGCCCTACTTGGTATATGTGC 496
QY 1143 CCGTGTGCGCTTTCGCTTGGAGCCCAAGATGGGAAAGGTGTGTTTGCAGTGGATGGGG 1202
Db 495 CCGTGTGCGCTTTCGCTTGGAGCCCAAGATGGGAAAGGTGTGTTTGCAGTGGATGGGG 436
QY 1203 AATTGATGTTAGCGAGCGCTGCGAGCCCAAGGTGCACCCAGCATGCTTCTGATGGTCA 1262
Db 435 AATTGATGTTAGCGAGCGCTGCGAGCCCAAGGTGCACCCAGCATGCTTCTGATGGTCA 376
QY 1263 GCGGTTGCTGGAGCGGCGGCGGCGAGCTGGAAGCCCGCAGATGCCACCGCAGAGAGC 1322
Db 375 GCGGTTGCTGGAGCGGCGGCGGCGAGCTGGAAGCCCGCAGATGCCACCGCAGAGAGC 316
QY 1323 CTTATGACCCCTTGGCGCGCTGTGCTTGTCTTACTTGCAGAGACCTTCTCTCTTC 1382
Db 315 CTTATGACCCCTTGGCGCGCTGTGCTTGTCTTACTTGCAGAGACCTTCTCTCTTC 256
QY 1383 CTTAGGCTGCGAGGCGCTGTCCAGAGCTCTGTGGGGTGGAGAGACTCTCTCTGGAGNA 1442
Db 255 CTTAGGCTGCGAGGCGCTGTCCAGAGCTCTGTGGGGTGGAGAGACTCTCTCTGGAGNA 196
QY 1443 GGGTGAAGAGTGGAGGCTATGCTTTGGGGGACAGGCCAGAAATGAAGTCTGGGTGAGG 1502
Db 195 GGGTGAAGAGTGGAGGCTATGCTTTGGGGGACAGGCCAGAAATGAAGTCTGGGTGAGG 136
QY 1503 AGCCAGCTGGCTGGCGCGCTGTGCTATGTAAGCGCTTCTAGTTTGTCTGAGACCGCC 1562
Db 135 AGCCAGCTGGCTGGCGCGCTGTGCTATGTAAGCGCTTCTAGTTTGTCTGAGACCGCC 76
QY 1563 ACCCCACGAAACCAATCCAAATAAAGTGACATTCCTCAA 1600
Db 75 ACCCCACGAAACCAATCCAAATAAAGTGACATTCCTCAR 38

RESULT 6

US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of

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/ FILE REFERENCE: 4-31617
/ CURRENT APPLICATION NUMBER: US/09/970,516
/ CURRENT FILING DATE: 2001-10-04
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1155
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1155)
/ OTHER INFORMATION:
/ JS-09-970-516-1

Query Match          70.3%;   Score 1124.6;   DB 9;   Length 1155;
Best Local Similarity 98.4%;   Pred. No. 8.6e-286;
Matches 1136;   Conservative 0;   Mismatches 19;   Indels 0;   Gaps 0;

2Y      176  ATGGATCAGCGGGCGGGCCCCCGGGGGGGTCTCCCGCGGCCCTTCGCGGTCTGGTGGTGGT 235
Db      1    ATGGATCAGCGGGCGGGCCCCCGGGGGGGTCTCCCGCGGCCCTTCGCGGTCTGGTGGTGGT 60
2Y      236  CTGAACCCGCGCGCGGGCAAGGCCCTTCGACGCTCTCCGGAGTCAGTGCAGGCC 295

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2y	296	CTTTTGGCTGAGGCTGAAATCTCTTTCACCTCATCTCTCACTGACGGCGGAAACACGCG	355
db	121	CTTTTGGCTGAGGCTGAAATCTCTTTCACCTCATCTCTCACTGACGGCGGAAACACGCG	180
2y	356	CGGAGCTGTGTGCGGTCCGAGGAGCTGGGCGCTGGGACGCTCTGTGTCTATGTCTTGA	415
db	181	CGGAGCTGTGTGCGGTCCGAGGAGCTGGGCGCTGGGACGCTCTGTGTCTATGTCTTGA	240
2y	416	CACTGGGCTGATGACGAGCTGTGTAACCGGCTCATATGACGCGCTGATGGGACGACCGCG	475

27 GACCGGCTGATGACGAGGTGTTGAACGGGCTCATGGACGGGCTGATGGGAGACCGGCC 300

2y 476 ATCCAGAGCCCTGTGTAGCTCCACAGGCTCTGSCAACGGCTGGCAGGTTCTTG 535

301 ATCCAGAGCCCTGTGTAGCTCCACAGGCTCTGGCAACGGCTGGCAGCTTCCTTG 360

536 AACCATTTATGCTGCTATGAGCAGGTCAACCAATGAAGACCTCCTGTACCAACTGCACGCTA 595

Db 361 AACCATATGCTGGCTATGAGCAGGTACCAATGAGAGACCTCCTGACCAACTGCACGCTA 420

QY 596 TTGCTGTGGCGCGCCGCTGTCAACCATGAACCTGTCTCTGCACACGGCTTCGGGG 655

D6	42T TTGCTGTGGCCCGGCCTGCTGTACCCCAATGAACCTTCCTGTCCTCAGCACACGGCTTCGGGG	#80
QV	656 CTGCGGCTGGTTCTCTGTGCTCTCAGCTTGCCCTGGGCGCTTCATTGTGATGTGGACTTAG	715

481 CTGCGCCTCTTCTCTGTGCTACGCTGGCCCTGGGGCTTCATTGCTGATGTGGACCTAGAG 540

Qy 716 AGTGATAGTATCGGGCTCTGGGGAGATGGCTTCACTCTGGGCACTTCTCGGCTCG 775

Db 541 AGTGAGAGTATCGGCGTCTGGGGGAGATCGGTTCACTCTGGGCACCTTCCTGCGTTG 600

QY 776 GCAGCCCTGCGGACCTTACCGCGGCCGATGGCTACCCCTCCTGTAGGAAGAGTGGGTTC 835

Db 601 GCAGCCCTGGCGACCTACCGCGGCCGACTGGCCCTACCTCCCTAGGAAGAGTGGGTTC 660

QY	836	AAAGACCTGCTTCTCCCCCGTGTGGTTCAGCAGAGGCCCCCGGTAGATGCAACACCTTGGTGGCA	895
D6	661	AATAGACA CTTTGCTCCCCCCCCCGTTGGTCTCAGCAGAGGCCCCGGTATATGTCACA CTTTGTGTGCA	720

QY 896 CTGGAGGACAGCTGCTCTCTACTGGCAGGTGGTCCCGACGAGGACTTTGTGCTAGTC 955

Db 721 CTGAGGAGCCACGTGCCCTCTCACTGGACAGTGTGCCGACGAGGACCTTTGTGCTAGTC 780

Qy 956 CTGGCACTGCTGCACCTGCACCTGGCCAGATGTTGCTGCACCCATGGCGCGTGT 1015

301 ATCCAGAGCCCTGTGTAGCTCCACAGAGGCTTGGCAAGCGCTTGGCAGCTTCCCTTG 360
536 AACCATTTATGCTGGCTATGAGCAGGTACCAATGAAGACCTCTCTGACCAACTGCACGCTA 595
361 AACCATTTATGCTGGCTATGAGCAGGTACCAATGAAGACCTCTCTGACCAACTGCACGCTA 420
596 TTGCTGTGGCGCGGCTGTGTACCATTAACCATTAACCATTAACCATTAACCATTAACCATTA 655
421 TTGCTGTGGCGCGGCTGTGTACCATTAACCATTAACCATTAACCATTAACCATTAACCATTA 480
656 CTGCGCTCGTTCCTGT 715
481 CTGCGCTCGTTCCTGT 540
716 AGTGATAAGTATCGGCGCTGTGGGAGATGCGGTTTCACTTCTGGGACACTTCTTGGCTGTG 775
541 AGTGATAAGTATCGGCGCTGTGGGAGATGCGGTTTCACTTCTGGGACACTTCTTGGCTGTG 600
776 GCAGCCCTCGGCACTTACCGCGCCGACTGGCTTACCTTCCCTGTAGGAAGAGTGGGTTTC 835
601 GCAGCCCTCGGCACTTACCGCGCCGACTGGCTTACCTTCCCTGTAGGAAGAGTGGGTTTC 660
836 AGACACCTGCTTCCCGCTGT 895
661 AGACACCTGCTTCCCGCTGT 720
896 CTGGAGGAGCAGTGGCTTCTCACTGCGCAGGTGCTGCGCGAGGAGTGTGTGTGTGTGTGTGT 955
721 CTGGAGGAGCAGTGGCTTCTCACTGCGCAGGTGCTGCGCGAGGAGTGTGTGTGTGTGTGTGT 780
956 CTGGCACTGCTGCACTCGCACTGGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1015
781 CTGGCACTGCTGCACTCGCACTGGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
1016 GCAGCTGGCGTATGATCTGT 1075
841 GCAGCTGGCGTATGATCTGT 900
1076 CGCCTCTCTCGGCCATGAGAAGGCGGCAATATGAGTATGATGATGATGATGATGATGATGAT 1135
901 CGCCTCTCTCGGCCATGAGAAGGCGGCAATATGAGTATGATGATGATGATGATGATGATGAT 960
1136 TATGTCCTGCTGTGCTTCCGCTTGGAGCCCAAGATGGAAGAGTGTGTGTGTGTGTGTGTGTGT 1195
961 TATGTCCTGCTGTGCTTCCGCTTGGAGCCCAAGATGGAAGAGTGTGTGTGTGTGTGTGTGTGT 1020
1196 GATGGGGAATTGATGTTAGCGAGCGCTGCGAGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1255
1021 GATGGGGAATTGATGTTAGCGAGCGCTGCGAGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
1256 ATGGTCAGCGGTTGCTGAGAGCCCGCCGCTGAGAGCCCGCCGCTGAGAGCCCGCCGCTGAGAG 1315
1081 ATGGTCAGCGGTTGCTGAGAGCCCGCCGCTGAGAGCCCGCCGCTGAGAGCCCGCCGCTGAGAG 1140
1316 GAAGAGCCCTTA 1327
1141 GAAGAGCCCTTA 1152

RESULT 8

JS-09-784-810A-3
: Sequence 3, Application US/09784810A
: Patent No. US20020082203A1
: GENERAL INFORMATION:
: APPLICANT: RASTELLI, LUCA
: TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
: FILE OF INVENTION: SAME
: FILE REFERENCE: 10716-08
: CURRENT APPLICATION NUMBER: US/09/784,810A
: PRIOR FILING DATE: 2001-02-14
: PRIOR APPLICATION NUMBER: 60/182,360
: PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-784-810A-3
Query Match 52.3%; Score 836.4; DB 9; Length 1759;
Best Local Similarity 72.8%; Pred. No. 5.4e-210;
Matches 1154; Conservative 0; Mismatches 411; Indels 21; Gaps 5;
QY 31 GGGGGGGAGAGGCGGCGCCACAGCGCGCTTGGAGCGCGCGCTTGGGAGCAGCCGATAA 90
DB 179 GAGGTGAGAGGGCGAGCCCAACGCGCAGTCCGACAGACACCTCTCTGGGCAACCCGATAA 238
QY 91 GGAGCTGAAGGAGGAGCGCGCG--CCAGGGGAGCGCGCGCCACACAGCGCGCAGGAGACCCC 147
DB 239 GAAGCTGAACGAGGAGCGCGCGTTACTCTTAGCAGCGCGCGGCGCAGCACGGTGGCGCC 298
QY 148 CTGCAAGCGGAGCGCGGTCGAGGTTATGATPCAGCGGGGCGCGCCCGGGGCGTGTCT 207
DB 299 TTGTACGCGGAGCGCGGACCTGGCTATGGAACCAAGTAGAATGCCCTCGAGGACTGCT 358
QY 208 CCGCGGCGCTGCGCGCTGT 267
DB 359 CCCAGGCGATGAGAGT 418
QY 268 GCAGCTTTCGGAGTCACGTGAGCGCGCTTTTGGTGTAGGCTGAAATCTCTCTTCACGCT 327
DB 419 GCAGCTTTCAGAGCGGT 478
QY 328 GATGCTCACTGAGCGGCGGAACCAACGCGCGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 387
DB 479 GATACTCACCAGAACGGAAGAACCATGCCAGGAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGT 538
QY 388 CTGGAGCGCTCTGT 447
DB 539 CTGGAGCGCTTGGCAGTCATGTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 598
QY 448 CATGGAGCGGCTGT 507
DB 599 AATGGAAACGCGCAGCTGTGGAGACTGCGCATCCAGAAACCCCTGTGTGTGTGTGTGTGTGT 658
QY 508 CTCTGGCAACGCGCTGCGCTTCTTTGAACCATATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 567
DB 659 CTCCGGCAATGCGCTGT 718
QY 568 TGAAGACCTCTGTGAACCACTGCAAGCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 627
DB 719 TGAAGACCTGTCTATCACTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 778
QY 628 CTCTGT 687
DB 779 CTGT 838
QY 688 GGGCTTCATTGT 747
DB 839 GGGCTTTGT 898
QY 748 CTTCACTCTGTGGGACCTTCTGT 807
DB 899 TTTCAAGTGTGGACCTTCTTGT 958
QY 808 TACCTCTCTGT 867
DB 959 CTACCTTCTGT 1015
QY 868 GGGCGCGGTAGTGCACACTGT 927
DB 1016 GGGCGCGGTGCACACACACTGT 1075

[illegible]

1018 GATGAGGCTGATGTATGTAAGTGTGTCAGGGCCCAAGTGCACCCAACTACCTTTGG 1077
1256 ATGGTCAGCGGTGGGTGGAGCCCGCCAGCTGGAAGCCCGCCAGCAGATGCCACCGCCA 1315
1078 ATGGTCTGTGGCAGCAGAGATGCCCCCATCCGCGCGGACTCCCGCGGGGCCACCTCCA 1137
1316 GAAGAGCCCTTA 1327
1138 GAAGAACCATAA 1149

RESULT 10
IS-09-954-456-1756/c
Sequence 1756, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1756
LENGTH: 394
TYPE: DNA
ORGANISM: Homo sapiens

IS-09-954-456-1756
Query Match 23.9%; Score 382.6; DB 9; Length 394;
Best Local Similarity 99.0%; Pred. No. 8.9e-91;
Matches 385; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1211 GTTAGGAGCGCGTCAGGGCCAGGTGCACCCAACTACTTCTGATGCTGAGCGGTGC 1270
394 GTTAGGAGCGCGTCAGGGCCAGGTGCACCCAACTACTTCTGATGCTGAGCGGTGC 335
1271 GTGAGAGCCCGCCAGCTGGAAGCCCGCAGCAGATGCCACCGCAGAGAGCCCTTATGA 1330
334 GTGAGAGCCCGCCAGCTGGAAGCCCGCAGCAGATGCCACCGCAGAGAGCCCTTATGA 275
1331 CCCCTGGGCGCGCTGTGCCTTAGTGTCTACTTGAGGACCGCTTCCCTTCCCTAGGGC 1390
274 CCCCTGGGCGCGCTGTGCCTTAGTGTCTACTTGAGGACCGCTTCCCTTCCCTAGGGC 215
1391 TCGAGGCGCTGTCCACAGCTCTCTGGGGTGGAGAGACTCCTCTGAGAGGGTGAGA 1450
214 TCGAGGCGCTGTCCACAGCTCTCTGGGGTGGAGAGACTCCTCTGAGAGGGTGAGA 155
1451 AGGTGGAGGCTATGCTTTTGGGGGGGACAGGCCAGAGATGAAGTCTGGGTGAGAGCCGAGC 1510

Db 154 AGTGGAGGCTATGCTTTGGGGGACAGCCACAATGAAGTCTGGGTGAGGAGCCAGC 95
Cy 1511 TGCGTGGGCCCACTGCTATGTAAAGCCTTCTAGTTTGTGTGAGACCCCGCCACG 1570
Db 94 TGGTGGGCCCACTGCTATGTAAAGCCTTCTAGTTTGTGTGAGACCCCGCCACG 35
Cy 1571 AACCAATCCAAATAAAGTGACATTCCCA 1599
Db 34 ACCAAATCCAAATAAAGTGACATTCCCA 6

RESULT 11
US-09-783-590-9248
Sequence 9248, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9248
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (68)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (193)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (220)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (221)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (236)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (289)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (297)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (337)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (350)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature
LOCATION: (356)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc feature

Query Match	16.1%;	Score 258;	DB 9;	Length 1857;
Best Local Similarity	63.3%;	Pred. No. 6.3e-58;		
Matches 396;	Conservative 0;	Mismatches 230;	Indels 0;	Gaps 0;
Qy	193	CCCCGGGGGGTCTCCCGGGCCCTCCGCGGTCGTGCTGCTGCTGAACCCGCGCGCGCGG	252	
Db	408	CACCCCTGACCTGTACTTCGGCGGCCCGGGTGTCTTCTATGGTCAATCCCTTTGGGG	467	
Qy	253	CRAAGGCGAAGGCCCTTCAGCTCTTCCGGAGTCACTGTGCAGCCCTTTGGCTGAGGCTGA	312	
Db	468	TCCGGGCGCTGGCCCTGGCAGTGGTGTAAAGAACCAACGCTGCTTCCCATGATCTCTGAAGCTGG	527	

528	GCTGTCTCTTAACCTCAT	CGAGCAGAA	CGACGAA	CCACGCC	CGGAGCGTGTCCAGGG	587
373	GGAGGAGCTGGGCGCTG	GGGACGCT	CTGTGTGTCATGT	CTGGAGACGGGCTGATGCACGA	432	
588	GCTGAGCCTGAGTGAGT	GGGATGGCAT	CGTCA	CGGTCTCGGAGACGGGCTGCTCCATGA	647	
433	GGTGTGTAAACGGGCTCA	TGAGGGGCGCTGACT	GGGAGACCGCCAT	CCAGAAAGCCCTGTG	492	
648	GGTGTCTAAACGGGCTCT	AGATGCCCTGACT	GGGAGGAGCTGT	GAGATGCTGTGGG	707	
493	TAGCTCCACAGAGGCTCT	GGGCAACCGGCTGGGAGCTT	CTCTTGAA	CCATATATGCTGGCTA	552	
708	CA ² CTCCCTCGGGT	CGGGCAACCGTGG	CGGAGCAGTGAAC	CGACACGGGGGATT	767	
553	TGAGCAGGTCAACCAATGA	AGACCTCTCTGACCAACT	GCACGCTATTGTGTCGCGCCCGCT	612		
768	TGAGCCAGCCCTGGGCGCT	CGACCTGTTGCTCAACT	GCTCACTGTTGTGTGCGGGGTGG	827		
613	GCTGTCACCCATGAAC	CTGTCTGTCTCTGCACACGGCTT	CGGGGCTGGCTCTCTCTGT	672		
828	TGSCACCACTGGA	CTGTCTCTCGGTGACGCTGGCC	CTCGGGTCCCGCTGTTCTCCTT	887		
673	GCTCAGCCTGGCCTGGGCTT	CAATTCCTGATGTGGACCT	TAGAGAGTGATAAATATCGGCG	732		
888	CCTGTCTGTGGCCTGGGCTT	CTGTGCAGATGTGGATAT	CCAGAGCGAGCGCTTCAGGGC	947		
733	TC ² TGGGGGAGATCGGCTT	CACTCTGGGCACTTCTCGCT	CTGGACCTCGGACCTTGGCACCTA	792		
948	CTTGGGAGTGGCCGCTT	CACTCTGGGACGCTGTGGGCT	CTGGCACCTGACACCTA	1007		
793	CCGCGGCGGACTGGCTAC	CCCTCCCTG	818			
1008	CCGCGGACGCTCTCTAC	CTCCCGG	1033			

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RESULT 13
US-09-817-676A-13
; Sequence 13, Application US/09817676A
; Patent No. US20020042101A1
; GENERAL INFORMATION:
; APPLICANT: Spiegel, Sarah
; APPLICANT: Kohata, Takafumi
; TITLE OF INVENTION: Mammalian Sphingosine 1
; TITLE OF INVENTION: Expression and Method
; FILE REFERENCE: 00170/HG
; CURRENT APPLICATION NUMBER: US/09/817,676A
; CURRENT FILING DATE: 2001-03-26

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GenCore version 5.1.1.6
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M protein - nucleic search, using frame_plus_p2n model

Run on: February 27, 2004, 11:04:46 ; Search time 101 Seconds

(without alignments)
2109.912 Million cell updates/sec

File: US-09-784-810C-2

Perfect score: 2015

Sequence: 1 MDPAGGPRGVLPKCRVLVL.....CVERPPSWKPPQMPPEEPL 384

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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MODE=LOCAL -OUTFMT=ptc -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000
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DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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- 2: /cn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	97.4	1155	US-09-970-516-1	Sequence 1, Appli
2	1927	95.6	1533	US-09-208-258-90	Sequence 90, Appli
3	1587.5	78.8	1149	US-09-970-516-5	Sequence 5, Appli
4	856.5	42.5	1857	US-09-970-516-3	Sequence 3, Appli
5	198	9.8	2462	US-09-620-312D-796	Sequence 796, App
6	147.5	7.3	915	US-09-134-000C-1961	Sequence 1961, Ap
7	130	6.5	978	US-09-107-532A-3132	Sequence 3132, Ap
8	127.5	6.3	4403765	US-09-103-840A-2	Sequence 2, Appli
9	126.5	6.3	4411529	US-09-103-840A-1	Sequence 1, Appli
10	125.5	6.2	894	US-09-134-000C-211	Sequence 211, App
11	118.5	5.9	942	US-09-107-532A-3500	Sequence 3500, Ap
12	113	5.6	900	US-08-961-527-332	Sequence 332, App

13	113	5.6	1035	4	US-09-134-000C-408	Sequence 408, App
14	110	5.5	1003	4	US-09-221-017B-1064	Sequence 1064, Ap
15	108	5.4	13542	4	US-08-956-171E-154	Sequence 154, App
16	106.5	5.3	1458	4	US-09-252-991A-14865	Sequence 14865, A
17	105	5.2	975	4	US-09-134-001C-1937	Sequence 1937, Ap
18	103.5	5.1	912	4	US-09-107-532A-1479	Sequence 1479, Ap
19	102.5	5.1	5092	3	US-09-412-545-1	Sequence 1, Appli
20	101	5.0	1548	4	US-09-252-991A-5880	Sequence 5880, Ap
21	99.5	4.9	2493	4	US-09-252-991A-12390	Sequence 12390, A
22	99.5	4.9	3024	4	US-09-252-991A-12202	Sequence 12202, A
23	99.5	4.9	111282	4	US-09-754-250-3	Sequence 3, Appli
24	98	4.9	22481	4	US-08-367-841A-43	Sequence 43, Appli
25	98	4.9	22481	5	PCT-US95-07201-43	Sequence 43, Appli
26	98	4.9	22484	4	US-09-875-223-2	Sequence 2, Appli
27	98	4.9	22484	4	US-09-875-114-2	Sequence 2, Appli
28	98	4.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
29	98	4.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
30	97	4.8	1131	4	US-09-252-991A-691	Sequence 691, App
31	97	4.8	3054	4	US-09-252-991A-720	Sequence 720, App
32	97	4.8	6885	4	US-09-252-991A-660	Sequence 660, App
33	96.5	4.8	5727	4	US-08-956-171E-190	Sequence 190, App
34	96	4.8	2657	4	US-09-495-050A-191	Sequence 191, App
35	96	4.8	23673	4	US-09-773-816-1	Sequence 1, Appli
36	95	4.7	1800	4	US-09-252-991A-12496	Sequence 12496, A
37	95	4.7	1956	4	US-09-252-991A-9165	Sequence 9165, Ap
38	95	4.7	36519	3	US-08-923-137-2	Sequence 2, Appli
39	94.5	4.7	1851	4	US-09-252-991A-9067	Sequence 9067, Ap
40	94.5	4.7	2849	4	US-09-866-028-77	Sequence 77, Appli
41	94.5	4.7	3681	4	US-09-581-105-1	Sequence 1, Appli
42	94	4.7	1617	4	US-09-252-991A-8802	Sequence 8802, Ap
43	94	4.7	1649	2	US-08-845-566-2	Sequence 2, Appli
44	94	4.7	2416	4	US-09-016-434-1058	Sequence 1058, Ap
45	94	4.7	536165	4	US-09-214-808-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-970-516-1
; Sequence 1, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1155)
; OTHER INFORMATION:
US-09-970-516-1

Alignment Scores:
Pred. No.: 1.54e-218 Length: 1155
Score: 1962.00 Matches: 375
Percent Similarity: 98.18% Conservative: 2
Best Local Similarity: 97.66% Mismatches: 7
Query Match: 97.37% Indels: 0
DB: 4 Gaps: 0

US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

Cy 1 MetAspProAlaGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
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Db 1 ATGATCCAGCGGCG 60
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
US-09-970-516-5

Alignment Scores:
Pred. No.: 61e-175 Length: 1149
Score: 1587.50 Matches: 302
Percent Similarity: 87.99% Conservative: 35
Best Local Similarity: 78.85% Mismatches: 45
Query Match: 78.78% Indels: 1
DB: 4 Gaps: 1

US-09-784-810C-2 (1-384) x US-09-970-516-5 (1-1149)

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QY 21 LeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
DB 61 CTGAACCCCGAGGGTGGCAGGGCAGAGGCTCTCGACCTCTTCAGAGCCGTGTGCAGCCC 120
QY 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgAsnHisAla 60
DB 121 TTCCTGGAGGAGGAGAGAGTAACCTTTAACTGATCTACCTACCTACCGAGGAGAACCATGCC 180
QY 61 ArgGluLeuValArgSerGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
DB 181 AGGAGCTGTGTGTGCAGAGGAGTGTGGGTCACTGGACGCTTGGCAGTCAATGCTGGT 240
QY 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
DB 241 GATGGTCTGATGATGAGGTGGTGAATGGCTAATGGAACGGCCGCTGAGAGCTGCC 300
QY 101 IleGlnLysProLysCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
DB 301 ATCCAGAAACCCCTGTGTAGCTCCCTCGAGGGTCCGCAATGGCTGGCAGCTTCTGTG 360
QY 121 AsnHisTyraGlyTyraGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
DB 361 AACCATATCTGGGTACGAGCAGGTGACTAATGAAGACCTGTCTCACTCACTGACACTG 420
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuSerLeuHisThrAlaSerGly 160
DB 421 CTGTTGTGCGCGCGGCGCTGTCAACCATGAACCTGTCTCTCCCTGCACACTGCTTCTGGG 480
QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
DB 481 CTGCGGCTCTATTCTGTGCTCAGTCTGTCTGGGGCTTTGTCTGCTGAGCTGACCTGAG 540
QY 181 SerAspLysTyraArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
DB 541 AGTGAGAAGTACAGGCGCTTGGGGGAGTTCGTTTTCACAGTGGGACCTTCTTTCGCTTA 600
QY 201 AlaAlaLeuArgThrTyraArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
DB 601 GCAAGCTCGGCGATCTACCAAGGCGCACTGGCTACTCTCTCTGTAGAACTGTGGCCTCT 660
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHisLeuValPro 240
DB 661 AAGAGACCCGCTCT---ACACTGGTGCAGAGGCGCCGCTGCACACACCTTGTCTCT 717
QY 241 LeuGluGlnValProSerHisTrpGlnValProAspGluAspPheValLeuVal 260
DB 718 CTGAGGAGGAGCAGTGCCTTCTCATTTGACTGTGTGTACCAAGACAGGAGCTTGTCTGTG 777
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QY 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
DB 778 CTGGTGTCTGTACACACCCACCTGAGCTCCGAGCTGTTTCAGACACCATGGGCGCTGT 837
QY 281 AlaAlaGlyValMetHisLeuPheTyraValArgAlaGlyValSerArgAlaMetLeuLeu 300
DB 838 GAGGCTGGTGTATGATGCTGTTCTAGCTAGCTGGGGGTGCAAGGGCTGCGCTGCTG 897
QY 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyraGluCysProTyraLeuVal 320
DB 898 GCGCTCTTCTGGCCATGCAAGGAGGAGCATATGGAACCTTGACTGTCCATACCTGCTT 957
QY 321 TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
DB 958 CATGTGCCGCTGGTGTGTTTCCGCTGGAGCCCGAGGAGGCGGTGTTTCTGTG 1017
QY 341 AspGlyGluLeuMetValSerGluAlaValGlnGlyGlnValHisProAsnTyraPheTrp 360
DB 1018 GATGAGGGCTGATGTTATGTGAAGCTGTGCAGGGCCAAAGTGACCCAACTACCTTTGG 1077
QY 361 MetValSerGlyCysValGluProProSerTrpLysProGlnGlnMetProProPro 380
DB 1078 ATGGTCTGTGCAGCAGAGATGCCCATCCGCGCGGAGCTCCCGCGGGGCGCCACTCCA 1137
QY 381 GluGluPro 383
DB 1138 GAAGAACA 1146
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RESULT 4

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US-09-970-516-3
; Sequence 3, Application US/09970516
; Patent No. 6610534
; GENERAL INFORMATION:
; APPLICANT: No. 6610534artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1857)
; OTHER INFORMATION:
US-09-970-516-3
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Alignment Scores:
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Score: 856.50 Matches: 189
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Best Local Similarity: 38.57% Mismatches: 111
Query Match: 42.51% Indels: 127
DB: 4 Gaps: 6
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US-09-784-810C-2 (1-384) x US-09-970-516-3 (1-1857)

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QY 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluLeuSerPhe 49
DB 478 GCGTGGCAGTGTGTAAAGAACCACTGCTTCCCATGATCTCTGAAGCTGGGCTGCTCTTC 537
QY 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
DB 538 AACCTCATCCAGACAGAACCGACAGACCGCGGAGGCTGGTCCAGGGGCTGAGCGCTG 597
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2Y 70 GlyArgTrrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValaen 89
2b 598 AETGAGTGGATGGATCGTACCGTCTCGGAGACGGGCTCTCCATGAGTGTCTGAC 657
2Y 90 GlyLeuMetGluArgProAspTrrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
2b 658 GGGCTCTAGATCGCCTGACTGGGAGGAGTGTGAAGATCCCTGTGGGCACTCTCCGCC 717
2Y 110 AlaGlySerGlyAsnAlaLeuAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
2b 718 TCGGGCTCGGGAACCGCTGGCCGAGAGTGAACACGACGGGGATTTGAGCCAGCC 777
2Y 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
2b 778 CTGGGCTCGACTGTGTCTCACTGCTCCTGTTGCTGTGCGGGGTGGTGGCCACCCA 837
2Y 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
2b 838 CTGGACCTGCTCTCCGTGACGCTGGCTCGGCTCCGGCTCCGGCTGTTCTCCTCTGCTGTGTG 897
2Y 170 AlaTrrpGlyPheIleAlaAspValAspLeuGluSerAspLysTyrArgGluGlyGlu 189
2b 898 GCGTGGGGCTTGTGTGATGTGATATCCAGAGCGAGCGCTTCAGGGCCCTTGGGCGAGT 957
2Y 190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
2b 958 GCCCGCTTCACACTGGGCAAGGTGTGGGCTTGGCCACTGCACACTACCGCGGAGCGC 1017
2Y 210 LeuAlaThrLeuProVal 215
2b 1018 CTCTCTACTCTCCCGCCACTGTGGAACCTGCTGGCCACCCCTGCGCATAGCCTGCGCT 1077
2Y 215 215
2b 1078 CGTGCAAGTCGAGCTGACCTTAACCCAGACCCAGCCGCCCATGGCCCATCACCC 1137
2Y 215 215
2b 1138 CTGCATCGTGTGTGTGCTGACCTGCTCTTCCTGTCGCCAGCCTGCGCTGCTCTCT 1197
2Y 215 215
2b 1198 GCGTCCAGAACCCCTGCCCATCTGTCCTCAACGGTGGGGGCCAGAGCTGGCTGGG 1257
2Y 215 215
2b 1258 GACTGGGTGGGCTGGGATGCTCGCTGTCCCGGACCCACTGCTGTCTTCACCTCTCT 1317
2Y 216 -----GlyArgValGlyPheLysThrProAlaSer-----ProValValValGln 230
2b 1318 GCGCTCTCCCAAGGCAGCTCTACACTCACCCGCTCTCCGAAGGGGCCCGGTAATCCGCCA 1377
2Y 231 Gln-----GlyPro 233
2b 1378 TCTCTGGGCTCCACTTCCACCTCCACCTGATGTCGGGTAGGGGCTTCCACCTGCGGCCG 1437
2Y 234 ValAspAlaHisLeuValProLeuGluGlnValProSerHisTrrpGlnValValPro 253
2b 1438 CCGACCCACTGCTGCTCGCTGGGACCCCGCTGCCAGACTGG---GTGACGCTG 1494
2Y 254 AspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPhe 273
2b 1495 GAGGGGAGCTTTGTGCTGTTGTCATCTGCGCCAGCCACTAGGCGCTGACTGTGTG 1554
2Y 274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
2b 1555 GCAGCTCCGATCGCGGCTTCGACGAGCGGCTGTGTGCACCTGTGTGGTGGGTAGCGGC 1614
2Y 294 ValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGlu 313
2b 1615 ATCTCGGGGCTGCGTGTGTGGGCTTTCTTGGCCATGAGCGGTGAGCCACTTCAGC 1674
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QY 314 TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAsp 333
Db 1675 CTGGGCTGTCCGAGCTGGGCTAGCGCGCGCCCGCTTCCGCTTAGAGCGCTCACA 1734
QY 334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
Db 1735 CCAGCGGCGTGTCTACAGTGGACGGGAGCAGGTGGAGTATGGCCGCTACAGGCACAG 1794
QY 354 ValHisProAsnTyrPheTrrpMetValSerGlyCysValGluProProProSerTrrpLys 373
Db 1795 ATGCACCTCGCATCGGTACACTGCTCACTGGG-----CCTCTGGCTGCG--- 1839
QY 374 ProGlnGlnMetProProProGluGluPro 383
Db 1840 -----CCGGGGCGGAGCCC 1854

RESULT 5
US-09-620-312D-796
; Sequence 796, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CJP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: Pt_FL_genes version 1.0
; SEQ ID NO 796
; LENGTH: 2462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(1464)
; US-09-620-312D-796

Alignment Scores:
Pred. No.: 1,24e-12 Length: 2462
Score: 198.00 Matches: 92
Percent Similarity: 41.02% Conservative: 77
Best Local Similarity: 22.33% Mismatches: 160
Query Match: 9.83% Indels: 83
DB: 4 Gaps: 18

US-09-784-810C-2 (1-384) x US-09-620-312D-796 (1-2462)
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Db 379 AAGGCCACTGTTTTCTTCATCTCTCAGCTTGCAGAGTGAAGGAAAGCCAGGACTCTATTGAA 438
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGlu 55
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JS-09-784-810C-2 (1-384) x US-09-134-000C-211 (1-894)

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19 CTCAAGCAACAAGAACTTAATATAGCGCTCTTACACTGATTACGCTGGACATGAAAAA 78
62 GluLeuValArg-----SerGluGluLeu----- 69
79 GAATTCAGCAAGAACTTCGACAAACAACTTACTCTCTGCTGAGACTTAGACGTT 138
70 GlyArgTrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
139 TCAACTTTCCATCCTAGTCTAGCTAGCGGCGATGGCACACTACATAATGCTATTAAT 198
90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
199 TCATTACTT-----CCATATGATTCATATTT-----CCTTAAGCTATATTCCTA 243
110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
244 TCGGGCTCTGGAATGATTTTGCACGAGGGGTTGATATACAGAAATATGATAAGCA 303
130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
304 TTGCATCAATCTGCGCACAGA-----CGACCA 333
150 MetAsnLeuLeuSerLeuHisThrAlaSer-----GlyLeuArgSer 163
334 AAGAAATTCAAACAACTTATGTAAAGCCACCAAGAAATCGCTTAGCCACC 393
164 PheSerVal-----LeuSerLeuAlaTrpGlyPheAlaAspValAspLeuGlu 180
394 AATAATGTTGGCTTAGGTTGGATGGCGCA-----ATCGTGGAAAAACCAACGAA 444
181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
445 TCGTCATCAAAAAAGCCCTTAAT-----AAATTTAAGCTTGGCTTCCTTATATTT 498
201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
499 TCTTCA-----ATCATTCATGCTCTTTT 522
221 LysThrProAlaSerProValValValGlnGlnGlyProVal-AspAlaHisLeuValPr 240
523 AGACAAAAAGGCTTTCCTCAATTTTAGTTGAATGAATGTTAAACAATACACATTTAATCGT 582
240 oLeu 241
583 GCTT 586

RESULT 11
US-09-107-532A-3500
Sequence 3500, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION ADDRESS:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GPC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3500:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...942
SEQUENCE DESCRIPTION: SEQ ID NO: 3500:
US-09-107-532A-3500
Alignment Scores:
Pred. No.: 0.000476 Length: 942
Score: 118.50 Matches: 53
Percent Similarity: 44.22% Conservative: 58
Best Local Similarity: 21.12% Mismatches: 89
Query Match: 5.88% Indels: 51
DB: 4 Gaps: 10
US-09-784-810C-2 (1-384) x US-09-107-532A-3500 (1-942)
QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysAlaLeuGlnLeuPheArg 35
DB 64 AAAGTTTATTAGTGTGTTAAACCCAGTTACGGCGGTGACACAGCA-----AAG 111
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe-----ThrLeuMet 52
DB 112 GAATTTGAGCAATTAGCGATAGCAAAATTCGAATCGGTGTTGATGAAGTGGTCTTG 171
QY 53 LeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrp 72
DB 172 CATACAAAAAAGCAGGGGATGCAAAAAATTTACTCGCAAGCGGTACGGAAGGTAT 231
QY 73 AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet 92
DB 232 CATAGTGTGTTGTCATGGCGGAGATGGAACAGTCAACGAGGAATCAGTGAATCGCT 291
QY 93 Glu-----ArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
DB 292 GAACAGAAACATCGGCCAAATTTCCGA-----TTTTTCCCA 327
QY 110 AlaGlySerGlyAsnAlaLeuAlaAspLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
DB 328 TTGGGTACGCTGATGACTTGGCTCGAGCATTAGGGATACCGCTAGACCTGAGGAAGCG 387
QY 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
DB 388 ATCAATCATTTTTCGATTGAATCA-----GTCAAGCCA 420
QY 150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
DB 421 TTGATATTCGAAAAATAAATAGAC-----CACTATTTTATGAATGTCGTC 465

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170 AlaTrpGlyPheIleAlaaspVal-----AspLeuGluSerAspLysTyrArgArgLeu 187
466 GCATTTGGCTCTATCCCTGAATCAATCAATGATGTAGATGGGAGAAAGACGAAATTT 525
188 GlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArg 207
526 GGAAAACTAGCTTATTTCATGTCAGGAATCAAACAGTTAGCTTCCACACAAATCCTACTCG 585
208 GlyArgLeu-----AlaThrLeuProValGly 216
586 TTTCAGTGAAGTGTATGGAAAGAGGAAGAAATTGACAGCAGTACTTCTGTATAGGA 645
217 ArgVal-----GlyPheLysThrProAlaSerProValValValGlnGlnGly 232
646 CTAACCTAATCAGTCGGCGGTTTGAACCATTTACTTCCAAATGCAAAAGTGGATGATCGT 705

RESULT 12
US-08-961-527-332/c
; Sequence 332, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 332:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-332

Alignment Scores:
Pred. No.: 0.00193 Length: 900
Score: 113.00 Matches: 47
Percent Similarity: 49.39% Conservative: 34
Best Local Similarity: 28.66% Mismatches: 54
Query Match: 5.61% Indels: 29
DB: 4 Gaps: 8

US-09-784-810C-2 (1-384) x US-08-961-527-332 (1-900)

```

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Db      472  AAAGCAATGGTAATATACCACTTACTTCTGGTGGCGAAGGCTTIG----- 425
Qy      36  SerHisValGlnProLeuLeuAlaGluAlaGluLeuSerPheThrLeuMet----- 52
Db      424  GATTACAAAGAAAGAGCTGGAGATAAAAGCAAAAGAATACTTTGAATATGTTGAAACCAA 365
Qy      53  LeuThrGluAArgAGenHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTTP  72
Db      364  ATTACCGAAAAGAGCGCTGGATGACACATTTTCTGCTGAAGAGCTTCTCGTGAGCAGTAT 305
Qy      73  AspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMet  92
Db      304  GATGCAGTGGTGTGTGTTGGTGGAGATGGAAGCTCAATCAAGTCAATTCAGGTATGAT 245
Qy      93  GluArgProAspTTPGluThrAlaIleGlnLysProLeuCysSerLeuProAlaGlySer 112
Db      244  GAGAGA---GACTAC-----ATTCTTAAG---TTAGGATTTATCCAGCGCGGTACG 200
Qy      113  GlyAsnAlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnValThrAsnGlu 132
Db      199  GGTAACTCATACAAAACCTTTTGGAA-----ATCAATCAAA 164
Qy      133  AspLeu-----LeuThrAsnCysThrLeu-----LeuLeuCysArg 144
Db      163  GACATCGATGGCGCAATTGACAACTGGATTTGATTAAACCAATGAATGATTCGGT 104
Qy      144  gProValLeuSerProMetAsnLeuSerLeuHisThrAlaSerGlyLeuArgSerPh 164
Db      103  AAAGCAAAATGACAACTATTTTGGTTATATCTTTAGTATCGGTTCTCTGCTGAGCGCAT 44
Qy      164  eSerValLeu 167
Db      43  CACAATGTG 34

RESULT 13
US-09-134-000C-408
; Sequence 408, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 408
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-408

Alignment Scores:
Pred. No.: 0.00242 Length: 1035
Score: 113.00 Matches: 71
Percent Similarity: 33.14% Conservative: 45
Best Local Similarity: 20.29% Mismatches: 132
Query Match: 5.61% Indels: 102
DB: 4 Gaps: 13

US-09-784-810C-2 (1-384) x US-09-134-000C-408 (1-1035)

Qy      19  ValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArgSerHisVal 38
Db      34  GTGATTATATATCCAACTCAGGAAAA-----GAGTTATCAATAAAGAACTTGA 81
Qy      39  GlnProLeuLeuAla-----GluAlaGluLeuSerPheThrLeu 51

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Qv 16 ArgValLeuValIleuLeuAsnProArgGlvGlvLvsGlvIvsAlaLeuGlnLeuPheArg 35
Db 82 GCGCATATTTTATCTATTTTGAAGAATGGTGTATGAAGCCAGTGCANTTGGCACC--- 138

16 ArgValLeuValLeuAsnProArgGlyLysGlyLysAlaLeuGlnLeupheArg 35

2Y 52 MetLeuThrCluArgArgAsnHisAlaArgGluLeuValArgSerGluCluLeuGlyArg 71
2b |||||
139 -----ACACCAGAGAAATTCAGCACCAATGAAGCACATCGTGCTCGCGGACAGA 192
2Y 72 TrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAengly--- 90
2b |||||
193 TTTGATTACTAGTACGCGGTGGAGATGGACCAATTAAGTCTGTGATGGATT 252
2Y 91 -----LeuMetGluArgProAspTrpGluThrAlaIleGlnIleProLeuCysSerLeu 108
2b |||||
253 GTCCTCGTGAAGCGGCGCCCT-----AAATGGCTATTATT 288
2Y 109 ProAlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyAlaGlyTyrGluGln 128
2b |||||
289 CCGTCTGGACGACGATGACTATGACCGGCGCTGAAG----- 327
2Y 129 ValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSer 148
2b |||||
328 -----ATTCTCTGTGATAATATCGTTAAGGCACGACAGTGAATAA 369
2Y 149 ProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSer 168
2b |||||
370 AAAATCAAACTGTCAAAATGATATGGCCAGCGGCAAAATTAATTTATCAATATT 429
2Y 169 LeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAspIleTyArgArgLeuGly 188
2b |||||
430 GCGCGGGTGGTCAATTAACGGAAGTCACTTATGAAGTTCCG----- 471
2Y 189 GluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaIleLeuArgThrTyrArgGly 208
2b |||||
472 -----TCAAGTGTGAAGTATTTTGTGT 495
2Y 209 ArgLeuAlaThrLeuProValGly-----ArgValGlyPheIleThrPro 223
2b |||||
496 TACTTAGCTACTTACCCAAAGAGCGGAAATGTGCCCGGAGTG----- 540
2Y 224 AlaSerProValVal-----ValGlnGlnGlyProValAsp 235
2b |||||
541 ----AAGCCGATTAATGGCATGACGTATGATGAAGGTGTGTACGAGGCAATCATCA 597
2Y 236 AlaHisLeuValProLeuGluGlnValProSerHisTrpGlnValValProAspGlu 255
2b |||||
598 ATGTTTTCTAGGGTCTACTAATCGGGTGGTGTGTTGACCAATCGTACCAT--- 654
2Y 256 AspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPheAlaAla 275
2b |||||
654 ----- 654
2Y 276 ProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyValArgAlaGlyValSer 295
2b |||||
655 -----GCTAAATTAGACGATGTAAGTTTTCATTAATCATTTGTAATAACAGCCCAATATT 708
2Y 296 ArgAlaValLeuLeuArgPheLeuAlaMetGluIleGlyArgHisMetGluTyrGlu 315
2b |||||
709 TTTGATTTCTTCAATTTAGTTCGTTAATGTTAATGTTGGAAGCATGTTGAACATCAT 768
2Y 316 CysProTyLeuValTyrValProValValAlaPheArgLeuGlu-----ProIleAsp 333
2b |||||
769 -----CGACTGATCTATACAAAGACGACGCTATTACATGTCAGAAACGTTAGAAAAGAAC 822
2Y 334 GlyIleGlyValPheAlaValAspGlyGlu 343
2b |||||
823 AATAAATGATTAATTTAGTGTGAA 852

RESULT 14

JS-09-221-017B-1064/c

Sequence 1064, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:

APPLICANT: ROSS, Bruce C.

TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USSES THEREOF

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gracys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1064:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...1003
US-09-221-017B-1064

Alignment Scores:
Pred. No.: 0.00514 Length: 1003
Score: 110.00 Matches: 82
Percent Similarity: 35.26% Conservative: 58
Best Local Similarity: 20.65% Mismatches: 139
Query Match: 5.46% Indels: 118
DB: 4 Gaps: 19

US-09-784-810C-2 (1-384) x US-09-221-017B-1064 (1-1003)

QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyGlyAlaLeuGlnLeuPheArg 35
2b |||||
Db 950 AAGATTCTAGCCATTATCAATNCCATATCGGGCATCGGATCG-----AAA 906
QY 36 SerHisValGlnProLeuLeuAlaGlu-----AlaGluIleSerPheThrLeuMetLeu 53
2b |||||
Db 905 AGCAACATACCGAGCCTTATAGCGGATGATTCCGCCCATCTCTCAGCACTCTTTATC 846
QY 54 Thr-----GluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArg 71
2b |||||
Db 845 ACCTATTGCAACGTGCTGCGCCATGCACTGTAATTGGCAGCACCAAGCAGTGGAGAAGCAT 786

QY 72 TrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAlaSerGlyLeu 91
DB 785 TACGACATGCGTATGCGATGAGGAGGATGGAACCGGTGAACGAGATAGCCCAAGGCTT 726
QY 92 MetGluArgProAspTyrGluThrAlaIleGlnLysProLeuLysCysSerLeuProAlaGly 111
DB 725 -----CGCTACCGATGATGCTGCTGGGTATGCTGCCCGAAGGA 687
QY 112 SerGlyAsnAlaLeuAlaSerLeuAsn----- 121
DB 686 TCAGCAACGGGTTTGGCAGCTGCCCTCAAGTCGCCATCACTCCGTCGGGAAGCTTCGAA 627
QY 122 ---HisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
DB 626 GTGATCAGAGCGGACATGTTCCGACC-----ATCGACTGCTGTGAA 585
QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
DB 584 CGCGATAGTCGCCCTTCTTTTGACACCTGCGGATTG----- 549
QY 161 LeuArgSerPheSerValLeuSerLeuAlaThrGlyPheIleAlaAspValAspLeuGlu 190
DB 548 -----CGATTCGATGCCGAGGT----- 531
QY 181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
DB 530 AGCAAGAAATTCGCCCAAGCGGGTAGTCGA----- 501
QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
DB 500 -----GCCCTATCACTTAT 486
QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAspAlaHis----- 237
DB 485 CGCGAACCATGATCGAGATTACTCCAAACGACGAGATCCAACTACGAGTAG 426
QY 238 ---LeuValProLeuGluGluGlnValProSerHisTyrPheValValProAspGluAs 256
DB 425 ACGCAAAATCTTTGAGGAGAAAGCTTTCTCGTCAC-----TTGGTGCA 380
QY 256 pPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPheAlaAlaPr 276
DB 379 -----ATGCCGCCCATGATGCGCAATACGCTTATATCGTCTC 342
QY 276 oMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly----- 293
DB 341 ATTAGCGGATTGCGAGGATGCTAAATGGATGTATTATTATCGTCTTCAATCCATT 282
QY 294 -ValSerArgAlaMetLeuLeuArgLeuPheLeu---AlaMetGluLysGlyArgHisMe 312
DB 281 GGAAGCTCCCAATTTGGCTTTTACAACTCTTTTACCAAGCGTATCAACAGCAACTCCCAATCT 222
QY 312 tGlu---TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluPr 331
DB 221 GGACACTATTAAGCCGGAACCTGATCAT-----GA 189
QY 331 oLysAspGlyLysGlyValPheAlaValAspGlyGlu-LeuMetValSerGluAlaValG 351
DB 188 CGGTGACAGACAGGCGGTATATGACCTCGATGCGGATCTGTCATGTCGGTAAAGCGCAT 129
QY 351 LngGlyGlnVal-----HisProAsnTyrPheTyrMetValSerGlyCysValG 367
DB 128 TGAGATCGGCACCTACGCGCGGTCACTCAGGTAATTG-----CTACTGAAACCTACACTTG 72
QY 367 luProProProSerTrp---LysProGlnGlnMetProProProGlu 381
DB 71 AAAGTCCCACTCTTTCTAATAAACCATAAATAAATCCCGTAACCGGAG 25

RESULT 15

US-08-956-171E-154/c
; Sequence 154, Application US/08956171E
; Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 13542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 154:
US-08-956-171E-154
Alignment Scores:
Pred. No.: 0.584 Length: 13542
Score: 108.00 Matches: 70
Percent Similarity: 25.52% Conservative: 60
Best Local Similarity: 19.13% Mismatches: 126
Query Match: 5.36% Indels: 110
DB: 4 Gaps: 18
US-09-784-810C-2 (1-384) x US-08-956-171E-154 (1-13542)
QY 16 ArgValLeuValLeuLeuAsnProArgGlyGlyLysAlaLeuGlnLeuPheArg 35
DB 5619 CGTGTAGATCATTTATTAACCCGACATCACTGATAA-----GAGCTATTATAA 5572
QY 36 SerHisValGlnProLeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGlu 55
DB 5571 -----AGAGATTACCTGATGCTTAATAAATTAGAA 5539
QY 56 ArgArgAsnHisAlaArgGluLeuValArgSerGluLeuLeuGly----- 70
DB 5538 AAAGCGGATATGAACGAGTGCATATGCAACCGGAAATAGGTGATGCCACTTGAA 5479
QY 71 -----ArgTrpAspAlaLeuValValMetSerGlyAspGlyLeu 83
DB 5478 GCAGAAAGAGCTATCCATGAAATATATGATGATATATCGCTGCAGGTGGTGGTGAACA 5419
QY 84 MetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLys 103

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5418 TTAATGAGTAGTAAATGGTATCGAGAAAGCCCTAAT-----CGTCCT 5374
2Y
104 ProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaAlaSerLeuAsnHisTyr 123
2b
5373 AAGCTAGGTGTCATCTCTATGGTACTGTTAATGACTTTGGACGTGCATTGCAT----- 5320
2Y
124 AlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuCys 143
2b
5319 -----ATACCTAATGAC----- 5308
2Y
144 ArgProValLeuSerProMetAsn---LeuLeuSerLeuHisThrAlaSerGlyLeuArg 162
2b
5307 -----ATCATGGGGCACTTCATGTCATCAATGAAGTCAATCTACTAAA----- 5263
2Y
163 SerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGluSerAsp 182
2b
5262 -----GTAGATATTGGTAAATGAATGAAT 5239
2Y
183 LysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAlaAla 202
2b
5238 CGATAC-----TTTATTAAATTTAGCTGCA 5215
2Y
203 LeuArgThrTyrArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLysThr 222
2b
5214 -----GGCGGACAATTGACG-----CAAGTCTCTTTATGAACA 5182
2Y
223 ProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValProLeuGlu 242
2b
5181 CCG---AGTAATTTGAAATCTATTGTTGTCATTT---GCTATTACATCAAGGTTTC 5128
2Y
243 GluGlnValProSer-----HisTrpGlnValVal 252
2b
5127 GAAATGTTACTCAATGAAAGCTGAGATTTAAGAAATGGAATATGATGCTAATGTTTC 5068
2Y
253 ProAspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMet 272
2b
5067 CAAGGAGAAGCATATTATTCTTTTGTAGTTTAAACAAATTCATGCGAGGATTGAAAAA 5008
2Y
273 PheAlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAla 292
2b
5007 TTA---GTCCGCGACGCTAAGTTAGATGACGGCTATTTTACGTTAATATATAGTTGAAAA 4951
2Y
293 GlyValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet 312
2b
4950 TCA---AACCTTGACAGAACTTGCTCATATTATGACTTTTAGCTTCAAGAGGAGACATACT 4894
2Y
313 GluTyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLys 332
2b
4893 AAGCAT-----CCTAAAGTTATTATGAAAAAGCAAGGCAATTAAATATTCATCA--- 4843
2Y
333 AspGlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGly 352
2b
4842 -----TTCACAGACTTACAACCTAAATGTTAGATGGAGAAATATGGTGGT 4801
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353 GlnValHisProAsnTyr 358
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4800 AAATTACCAGCGAATTC 4783

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Search completed: February 27, 2004, 22:07:57
Job time : 2740 secs

GenCore version 5.1.1.6
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M protein - nucleic search, using frame_plus_p2n model

Run on: February 27, 2004, 20:01:08 ; Search time 397 Seconds
(without alignments)
3489.338 Million cell updates/sec

Title: US-09-784-810C-2
Perfect score: 2015
Sequence: 1 MDPACGPRGLPRPCRVLV.....CVERPPSKPQMPPEPL 384

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 2353733 seqs, 1803733377 residues
Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications_NA:
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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	Query	%
No.	Score	Match Length DB ID Description

1	2015	100.0	1600	9	US-09-784-810A-1	Sequence 1, Appli
2	1962	97.4	1152	15	US-10-348-052-22	Sequence 22, Appl
3	1962	97.4	1155	9	US-09-970-516-1	Sequence 1, Appli
4	1962	97.4	1799	14	US-10-354-358-25	Sequence 25, Appl
5	1944	96.5	1562	15	US-10-264-237-1180	Sequence 1180, Ap
6	1927	95.6	1533	10	US-09-933-767-90	Sequence 90, Appl
7	1927	95.6	1533	14	US-10-023-282-90	Sequence 90, Appl
8	1594.5	79.1	1759	9	US-09-784-810A-3	Sequence 3, Appli
9	1587.5	78.8	1143	9	US-09-970-516-5	Sequence 5, Appli
10	875	43.4	2698	9	US-09-817-676A-11	Sequence 11, Appl
11	856.5	42.5	1857	9	US-09-970-516-3	Sequence 3, Appli
12	856.5	42.5	2380	9	US-09-817-676A-13	Sequence 13, Appl
13	856.5	42.5	2380	14	US-10-354-358-77	Sequence 77, Appl
14	550	27.3	2629	15	US-10-348-052-24	Sequence 24, Appl
15	492.5	24.4	2609	15	US-10-348-052-25	Sequence 25, Appl
16	481	23.9	480	9	US-09-783-590-9248	Sequence 4748, Ap
17	444.5	22.1	2084	12	US-10-424-599-47396	Sequence 47396, A
18	427	21.2	1869	12	US-10-425-114-34806	Sequence 34806, A
19	365	18.1	296	9	US-09-777-564-658	Sequence 658, App
20	365	18.1	296	14	US-10-015-219-658	Sequence 658, App
21	360	17.9	199	9	US-09-796-692-2905	Sequence 2905, Ap
22	360	17.9	199	14	US-10-040-862-2905	Sequence 2905, Ap
23	360	17.9	199	15	US-10-057-475B-2905	Sequence 2905, Ap
24	360	17.9	199	15	US-10-154-884B-2905	Sequence 2905, Ap
25	305.5	15.2	832	14	US-10-029-386-20952	Sequence 20952, A
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28	273	13.5	2014	12	US-10-424-598-59419	Sequence 59419, A
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30	268.5	13.3	4413	10	US-09-969-898-16	Sequence 16, Appl
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32	266.5	13.2	4432	15	US-10-120-988-148	Sequence 148, App
33	260.5	12.9	4463	14	US-10-315-597A-1	Sequence 1, Appli
34	255	12.7	1840	9	US-09-784-810A-5	Sequence 5, Appli
35	228	11.3	394	9	US-09-954-456-1756	Sequence 1756, Ap
36	223	11.1	979	10	US-09-969-898-1	Sequence 1, Appli
37	221	11.0	639	15	US-10-260-238-964	Sequence 964, App
38	213.5	10.6	1949	15	US-10-260-238-1212	Sequence 1212, Ap
39	206	10.2	4004	10	US-09-814-353-13777	Sequence 13777, A
40	198	9.8	2462	14	US-10-037-270-796	Sequence 796, App
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44	184.5	9.2	1632	12	US-10-424-599-10078	Sequence 10078, A
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 1
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)


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161 LeuArgSerPheSerValLeuSerLeuAlaThrGlyPheIleAlaAspValAspLeuGlu 180
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481 CTGCGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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181 SerAspLysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
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661 AGACACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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241 LeuGluGlnValProSerHisTyrGlnValValProAspGluAspPheValLeuVal 260
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261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
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301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
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RESULT 3

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GENERAL INFORMATION:
APPLICANT: No. US20020099029A1artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
poly nucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1155
TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1155)
OTHER INFORMATION:
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Score: 1922.00
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US-09-784-810C-2 (1-384) x US-09-970-516-1 (1-1155)

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Qy 61 ArgGluLeuValArgSerGluGluLeuGlyArgTyrAspAlaLeuValMetSerGly 80
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Qy 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTyrGluThrAla 100
Db 241 GACGGGCTGATGACGAGGTGTGTGACGGGCTCATGGAGCGGCTGACTGGGAGACGCG 300
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Qy 121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuThrAsnCysThrLeu 140
Db 361 AACATTATGCTGGCTATGAGCAGGTCCACCAATGAAGACCTCTCTGACCAACTGCACGCTA 420
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; Sequence 25, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lescon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 7103, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2039,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 6428 MOLECULES
; FILE REFERENCE: MPI02-020P1RNONMIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1799
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (359)...(1513)
US-10-354-358-25

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Score: 1962.00 Matches: 375
Percent Similarity: 98.18% Conservative: 2
Best Local Similarity: 97.66% Mismatches: 7
Query Match: 97.37% Indels: 0
DB: 14 Gaps: 0

US-09-784-810C-2 (1-384) X US-10-354-358-25 (1-1799)

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QY 21 LeuAsnProArgGlyGlyLysAlaLeuGlnLeuPheArgSerHisValGlnPro 40
Db 419 CTGAACCCCGCGGGCGGCAAGGCAAGCCCTTGACGCTCTTCCGGAGTCAGTCGAGGCC 478
QY 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
Db 479 CTTTGGGTGAGGCTGAATCTCTTACGCTGATGCTCACTGAGCGGCGGAACCCAGCG 538
QY 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAlaLeuValValMetSerGly 80
Db 539 CGGGAGCTGGTGGTGGGAGAGTGGCGCGCTGGGACGCTCTGGTGGTCTGTGTGTGGA 598
QY 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
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QY 241 LeuGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
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; Sequence 90, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
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; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1522)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1527)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-933-767-90
Alignment Scores:
Pred. No.: 2,37e-230 Length: 1533
Score: 1927.00 Matches: 371
Percent Similarity: 96.88% Conservative: 2
Best Local Similarity: 96.38% Mismatches: 11
Query Match: 95.63% Indels: 1
DB: 10 Gaps: 0


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/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,374
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,917
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,949
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,883
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,897
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,898
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,962
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,963
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,877
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,878
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/070,923
/ EARLIER FILING DATE: 1997-12-18
/ EARLIER APPLICATION NUMBER: 60/092,921
/ EARLIER FILING DATE: 1998-07-15
/ EARLIER APPLICATION NUMBER: 60/094,657
/ EARLIER FILING DATE: 1998-07-30
/ NUMBER OF SEQ ID NOS: 1227
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 90
/ LENGTH: 1533
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (12)
/ OTHER INFORMATION: n equals a.t,g, or
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (123)
/ OTHER INFORMATION: n equals a.t,g, or
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1522)
/ OTHER INFORMATION: n equals a.t,g, or
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (1527)
/ OTHER INFORMATION: n equals a.t,g, or
/ PS-10-023-282-90

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; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; FILE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-784-810A-3

Alignment Scores:
Pred. No.: 1,08e-188 Length: 1759
Score: 1594.50 Matches: 303
Percent Similarity: 88.25% Conservative: 35
Best Local Similarity: 79.11% Mismatches: 44
Query Match: 79.13% Indels: 1
DB: 9 Gaps: 1

US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1759)

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2b 327 ATGGAACCAAGTAGAATGCCCTCGAGAGCTGCTCCACAGGCCATGCAGAGTGTGCTG 386
2y 21 LeuAsnProArgGlyGlyValLeuValLeuValLeuValLeuValLeuValLeu 40
2b 387 CTGAACCCAGGCTGCGAGGCAAGGCTGTCAGCTCTTCCAGAGCGGTGTCAGGCC 446
2y 41 LeuLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
2b 447 TTCTCTGGAGGAGCAGAGATAACCTTTAACTGATACCTACCGACGGAAGAACCATGCC 506
2y 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValValMetSerGly 80
2b 507 AGGAGCTGCTGTGTCAGAGAGTTGGGTCTACTGCGGACGCCCTCGCAGTCTATGTCGGT 566
2y 81 AspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
2b 567 GATGGTCTGATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
2y 101 IleGlnProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
2b 627 ATCCAGAAACCCCTGTAGTACCTCCCTGGAGGCTCCGCAATGCTGCGAGCTTCTGTG 686
2y 121 AsnHisTyAlaGlyTyArgGluValThrAsnGluAspLeuThrAsnCysThrLeu 140
2b 687 AACCATATGCTGGTACGAGCAGAGTGTATGAGACCTGCTCATCACTGACACTG 746
2y 141 LeuLeuCysArgProValLeuSerProMetAsnLeuSerLeuHisThrAlaSerGly 160
2b 747 CTGTTGTGCGCGCGGCGCTGTACCCATGAACCTGTCTCCCTGCACACTGCTTCTGGG 806
2y 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAspLeuGlu 180
2b 807 CTGCGGCTCTATTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 866
2y 181 SerAspLysTyArgArgLeuGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
2b 867 AGTGAGAGTACAGGCGCTTGGGGAGATTCCTTTCACAGTGGGCACTTCTTTCGCTA 926
2y 201 AlaAlaLeuArgThrTyArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPhe 220
2b 927 GCAAGCCTGCGATCTACCAAGGCCCACTGGGCTACCTTCTCTAGGAACCTGTGCGCTCT 986

; LysThrProAlaSerProValValValGlnGlnGlyProValAspAlaHisLeuValPro 240
; 987 AAGAGACCGGCTCT--ACACTGGTGAGAAAGGCGCCGCTCGACACACACTTGTCTCT 1043
;
; LeuGluGluGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
; 1044 CTGAGAGGAGCCAGTGCCTCTCTCATGTGACTGTGTGTACAGACAGGACTTCTGCTG 1103
;
; LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCys 280
; 1104 CTGGTGTCTGTACACACCCACCTGAGCTCCGAGCTGTTTTCAGCAGCCATGGCGCTGT 1163
;
; AlaAlaGlyValMetHisLeuPheTyValArgAlaGlyValSerArgAlaMetLeuLeu 300
; 1164 GAGCTGTGTATGTCATCTCTTCTACGTAGTCCGGGGGTGTCAGGGCTGCGCTCTG 1223
;
; ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyTrpGluCysProTyTrpLeuVal 320
; 1224 CGCTCTTCTCTGGCCATGCAGAGGCAAGCATATGGAATCTGACTGTCCATACCTGTT 1283
;
; TyrValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaVal 340
; 1284 CATGTGCGCGTGTGTGCTTTCGCTCGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 1343
;
; AspGlyGluLeuMetValSerGluAlaValGlnGlnValHisProAsnTyPheTrp 360
; 1344 GATGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1403
;
; MetValSerGlyCysValGluProProSerTrpLysProGlnGlnMetProProPro 380
; 1404 ATGCTCTGTGCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
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; 381 GluGluPro 383
; 1464 GAGAACCA 1472

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; Sequence 5, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE OF INVENTION: polynucleotides encoding sphingosine kinases
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 5
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
; US-09-784-810C-2 (1-384) x US-09-784-810A-3 (1-1149)

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Pred. No.: 4.28e-188 Length: 1149
Score: 1587.50 Matches: 302
Percent Similarity: 87.99% Conservative: 35
Best Local Similarity: 78.85% Mismatches: 45
Query Match: 78.78% Indels: 1
DB: 9 Gaps: 1

; 1 MetAspProAlaGlyGlyProArgGlyValLeuProArgProCysArgValLeuValLeu 20
; 1 ATGGAACCAAGTAGAATGCCCTCGAGAGCTGCTCCACAGGCCATGCAGAGTGTGCTGCTG 60
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QY 61 CTGAACCCCGAGGGTGGCAAGGGCAAGGCTCTGAGAGCTCTCCAGAGCCGTGTGAGCCC 120
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QY 41 LeuLeuAlaGluAlaGluIleSerPheThrLeuMetLeuThrGluArgArgAsnHisAla 60
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QY 121 TTCCTGAGGAGGAGAGATACCTTTAACTGATCTACCCGACGGAAGAACCATGCC 180
Db
QY 61 ArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeuValMetSerGly 80
Db
QY 181 AGGAGCTGGTGTGTCAGAGAGGTGGGTACCTGGAGACCCCTGGCAGTCATGTCGGT 240
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QY 81 AspGlyLeuMetHisGluValValAlaAsnGlyLeuMetGluArgProAspTrpGluThrAla 100
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QY 241 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
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QY 101 IleGlnIysProLeuCysSerLeuProAlaGlySerGlyAsnAlaLeuAlaSerLeu 120
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QY 301 ATCCAGAAACCCCTGTAGCTCCCTGGAGGCTCCGGCAATCGCTGGCAGCTTCTGTG 360
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QY 121 AsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeu 140
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QY 141 LeuLeuCysArgProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGly 160
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QY 421 CTGTTGTGCGCGCGCGCTGTCCACCATGAACCTGCTGCCCTGCACACTGCTTCTGGG 480
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QY 161 LeuArgSerPheSerValLeuSerLeuAlaTrpGlyPheIleAlaAspValAlaLeuGlu 180
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QY 481 CTGCGGCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
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QY 181 SerAspIysTyrArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeu 200
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QY 541 AGTCAGAAAGTACAGCGCTTGGGGGAGATCTGTTTACAGTGGGCACTTCTTTCGCTA 600
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QY 201 AlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeuPheValGlyArgValGlyPhe 220
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QY 601 GCAAGCTGGCACTACCAAGGCACTGGCTACCTTCTCTAGAACTGTGGGCTCT 560
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QY 221 LysThrProAlaSerProValValGlnGlnGlyProValAlaAspAlaHisLeuValPro 240
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QY 661 AAGAGACCCGCTCT---ACACTGGTGCACAGAGGCGCCCTGCACACACACCTTGTCT 717
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QY 241 LeuGluGlnGlnValProSerHisTrpGlnValValProAspGluAspPheValLeuVal 260
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QY 718 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 777
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QY 261 LeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAlaProMetGlyArgCys 280
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QY 778 CTGGTGTGTGTACACACACACCTGAGCTCCGAGCTGTTTGCACACACCCATGGCCCTGT 837
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QY 281 AlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSerArgAlaMetLeuLeu 300
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QY 838 GAGGCTGGTGTATGATCTGTTCTAGCTACGTGCGGGGGGTCAAGGGGTGCGCTGCTG 897
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QY 301 ArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyrGluCysProTyrLeuVal 320
Db
QY 898 CGCTCTTCTCCGCGCATGCGAAGGGCAAGCATATGGAATTCAGCTGTCATACCTGGTT 957
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QY 321 TyrValProValAlaAlaPheArgLeuGluProIlysAspGlyLysGlyValPheAlaVal 340
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QY 958 CATGTGCCCGTGGTGTCTTCCGCTCGAGGCCAGAGGCCGAGGGGGGTCTTCTGTG 1017
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QY 361 MetValSerGlyCysValGluProProProSerTrpIysProGlnGlnMetProProPro 380
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Db

QY 381 GluGluPro 383
Db
Db 1138 GAAGAACCA 1146
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US-09-817-676A-11
US-09-817-676A-11 Application US/09817676A
Patent No. US20020042101A1
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
CURRENT APPLICATION NUMBER: US/09/817,676A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 2698
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (387)..(2237)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization of a
TITLE: novel mammalian sphingosine kinase type 2 isoform
JOURNAL: J. Biol. Chem.
VOLUME: 275
ISSUE: 26
PAGES: 19513-19520
DATE: 2000-06-30
DATABASE ACCESSION NUMBER: AF245448
DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-11
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Pred. No.: 1,84e-98 Length: 2698
Score: 875.00 Matches: 187
Percent Similarity: 51.98% Conservative: 63
Best Local Similarity: 38.98% Mismatches: 111
Query Match: 43.42% Indels: 120
DB: 9 Gaps: 4
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Db 867 GCCTGGCAGCGCTGTATGACACAGCTGTGTCACATGATCTCTGAAGCTGGGCTGCTCCTTC 926
QY 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
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Db 927 AACCTCATACAGACAGACAGACCATCCCTGAGCTGGTGAGGGGTTAAGCTG 986
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Db 987 AGTGAGTGGGAAGGCATGTCTACCTGTGTCTGACACGGCTGCTTACGAGGTCTGTAAT 1046
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QY 110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
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Db 1107 TGTGATCGGCAATGCTAGCTAGCTGGGCGGTGAGCCATCATGCGGGTTTGACAGGTT 1166
Db


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2Y 150 MetAsnLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
2b 1227 CTGGACTTCTCTCTGACGCTAGCTCGGATCCGCTGTTTCTCTCTGTCAGTG 1286
2Y 170 AlaTrpGlyPheLeuAlaAspValLeuGluSerAspLysTyrArgArgLeuGlu 189
2b 1287 GCTCGGGATTCTGTCAGATGGACATTCACAGTAGCGCTTCAGGGCCCTGGGAGC 1346
2Y 190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
2b 1347 GCTCGATTACACTGGGTGACGTAGTGGCTGGCTGCTGCTGCTGCTGCTGCTG 1406
2Y 210 LeuAlaThrLeuProVal----- 215
2b 1407 CTCTCTACTCTCCCTACACAGAACAGCGTTGCCCATCCAGGCGCACAGTCTGCGT 1466
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2Y 217 ArgValGlyPheLysThrPro-----AlaSerProValValGlnGlnGlyProVal 234
2b 1767 TCTTGGGGTTCTGCTGCTCCACCCAGCTGCTCCCTCAATGGTGGTGGTCCAGAGCTGACT 1826
2Y 235 AspAlaHisLeuValProLeuGluGlnValProSerHisTrpGlnValValProAsp 254
2b 1827 GACCACTCTCTCTCTCTGCTGCTCTCCACTGCTCCAGCTGCTGCTGCTGCTGCTGCTG 1886
2Y 255 GluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPheAla 274
2b 1887 GAG----TTTGTACTATGTTGGGATCTTTGACGAGCCACCTCTGCGCAGACCTGATGCA 1943
2Y 275 AlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyVal 294
2b 1944 GCCCCACATGACGCTTTGATGATGGCTGTGGCTGTGACCTGTGTGGTGGGAGCGGATC 2003
2Y 295 SerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGluTyr 314
2b 2004 TCACGGGCTGCACTTCTACGCAATTTTCTGGCCATGGAGCATGGAACCACTTCAGCCTG 2063
2Y 315 GluCysProTyrLeuValTyrValProValAlaPheArgLeuGluProLysaspGly 334
2b 2064 GGTGCCCCCATCTGGGCTATGCTGACGACGCTGCTTCCGCTTTGACCTTGAACCACTCAGGCT 2123
2Y 335 LysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlnVal 354
2b 2124 CGTGGCTGCTCACTGATAGTGGAGTGTAGTGGAGTATGGGCCCAATACAGCGCAGGTG 2183
2Y 355 HisProAsnTyrPheTrpMetValSerGlyCysValGluProProSerTrpLysPro 374
2b 2184 CACCCAGGCTCGCCACGCTGCTACTGGG-----CCTGCAGGTCAAAAGCCA 2231
2Y 375 Gln 375
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Db 2232 CAA 2234

RESULT 11

US-09-970-516-3
; Sequence 3, Application US/09970516
; Patent No. US20020099029A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020099029A1artis AG
; TITLE OF INVENTION: Induction of blood vessel formation through administration of
; FILE REFERENCE: 4-31617
; CURRENT APPLICATION NUMBER: US/09/970,516
; CURRENT FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 1857
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1857)
; OTHER INFORMATION:
US-09-970-516-3

Alignment Scores:
Pred. No.: 2,16e-96 Length: 1857
Score: 856.50 Matches: 189
Percent Similarity: 51.43% Conservative: 63
Best Local Similarity: 38.57% Mismatches: 111
Query Match: 42.51% Indels: 127
DB: Gaps: 6

US-09-784-810C-2 (1-384) x US-09-970-516-3 (1-1857)

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Db 478 GCTGGGAGTGGTGTAAAGACCACTGCTTCCCATGATCTCTGAAGCTGGGCTGCTCTTC 537
QY 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
Db 538 AACCTATCCAGACAGAACACAGACACCGCGGAGCTGTCAGGGGCTGAGGCTG 597
QY 70 GlyArgTrpAspAlaLeuValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
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QY 90 GlyLeuMetGluArgProAspTrpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
Db 658 GGGCTCTAGATGGCTGTGAGAGAGAGCTGTGAGATGCTGTGGGCATCTCTCCC 717
QY 110 AlaGlySerGlyAsnAlaLeuAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
Db 718 TGGCGCTCGGCAACGCGCTGGCGGAGCAGTGAACACAGCACGGGGGATTTGAGCCAGCC 777
QY 130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
Db 778 CTGGGCTCGACCTGTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
QY 150 MetAsnLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
Db 838 CTGGACCTGCTCTCGGTGACGCTGGCGCTCGGCTGCTGCTGCTGCTGCTGCTGCTG 897
QY 170 AlaTrpGlyPheLeuAlaAspValLeuGluSerAspLysTyrArgArgLeuGlyGlu 189
Db 898 GCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 957
QY 190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
```



```

964 GCGCGCTTCACACTGGGACGGTGTGGGCTTGGCCACTGCACACTGACCGGACGC 1023
210 LeuAlaThrLeuProVal
1024 CTCCTCTACCTCCCGCCCACTGTGGAACTGCTGCGCCACCCCTGCCATAGCTGTGCT 1083
215 -----
215 -----
1084 CPTGCCAAGTCGAGCTGACCTTAACCCAGACCCGCGCCATGGCCCACTCACCC 1143
215 -----
215 -----
1144 CTGATCGTCTGTGTCGACCTGCTTTCCTCTGCCAGCCTGCCCTGGCCTCTCTCT 1203
215 -----
215 -----
1204 GGTGCGCAGAACCCCTGCCATCTCTCTCAAGGTGGGGGCCAGAGCTGTGGTGG 1263
215 -----
215 -----
1264 GACTGGGGTGGGGCTGGGATGCTCGCTGTCCCGGACCCACTGCTCTTCACTCTCT 1323
215 -----
215 -----
216 -----GlyArgValGlyPheLysThrProAlaSer-----ProValValValGln 230
1324 GGTCTCCACAGACGCTTACACTACCCCTGTCCGAAGGGGGCCCGTAATCCCCCA 1383
231 Gln-----
1384 TCTCTGGCTCCCACTTCCCACTGATGCTGCGGTAGGGGCTCCACCTGCGGCCCG 1443
234 ValAspAlaHisLeuValProLeuGluGluInValProSerHisTirpGlnValValPro 253
1444 CCGGACCACTCTGCTCGCTCGCTGGGACCCCGCTGCCAGAGCTGG---GTGAGCGTG 1500
254 AspGluAspPheValLeuValLeuAlaLeuLeuHisSerHisLeuAlaSerGluMetPhe 273
1501 GAGGGGACTTTGTCTCATGTGTCATCTGCGCATCTGCCAGCCACTAGGCGCTGACCTGTG 1560
274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGly 293
1561 GCAGCTCCGATCGCGCTGTCGACGACGCGCTGTGTCACCTGTGCTGGTGGCTAGCGGC 1620
294 ValSerArgAlaMetLeuLeuLeuGluPheLeuAlaMetGluLysGlyArgHisMetGlu 313
1621 ATCTCGGGGCTGGCTGTGCTGCGCTTTCTTGGCATGGAGCGGTATGGCCCTACAGCCACG 1680
314 TyrGluCysProTyrLeuValTyrValProValAlaPheArgLeuGluProLysAsp 333
1681 CTGGGCTGTCCGAGCTGGGCTACCGCGCGCGCTTCCGCTTAGCGGCTCACA 1740
334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
1741 CCACGCGGCTGTCTCACAGTGGACGGGAGAGGTGGAGTATGGCCCTACAGCCACAG 1800
354 ValHisProAsnTyrPheTirpMetValSerGlyCysValGluProProProSerTirpLys 373
1801 ATGCACCTTGGATCGGTACATGCTCACTGGG-----CTTCTGGGTGC----- 1845
374 ProGlnGlnMetProProGluGluPro 383
1846 -----CCGGGGGGGGAGGCC 1860
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RESULT 13

US-10-354-358-77

Sequence 77, Application US/10354358

Publication NO. US20030157082A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Hunter, John Joseph

APPLICANT: MacBeth, Kyle J.

APPLICANT: Tsai, Fong-ying

APPLICANT: Lesoon, Andrea

APPLICANT: Lightcap, Eric S.

```

APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REFERENCE: ME102-020PKNOMNIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 2380
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (7)...(1863)
US-10-354-358-77
Alignment Scores:
Pred. No.: 3,13e-96 Length: 2380
Score: 856.50 Matches: 189
Percent Similarity: 51.43% Conservative: 63
Best Local Similarity: 38.57% Mismatches: 111
Query Match: 42.51% Indels: 127
DB: 14 Gaps: 6
US-09-784-810C-2 (1-384) x US-10-354-358-77 (1-2380)
Qy 10 ValLeuProArgProCysArgValLeuValLeuAsnProArgGlyLysGlyLys 29
Db 424 CTGCTACTCGCGCGCCCGCTTCTTATTTGTCATCCCTTTGGGGTGGGGCTG 483
Qy 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluIleSerPhe 49
Db 484 GCCTGGCAGTGGTGAAGAACACACGCTCTCCCATGATCTCTGAAGCTGGGCTCTCCTTC 543
Qy 50 ThrLeuMetLeuThrGluArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeu 69
Db 544 AACCTCATCCAGACAGACACAGAACACACGCGCGGAGCTGTGTCAGGGGCTGAGCCTG 603
Qy 70 GlyArgTirpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluValValAsn 89
Db 604 AGTGAGTGGGATGGCATCTGTCACGGTCTCGGGAGACGGGCTGCTCATGAGGTGCTGAAC 663
Qy 90 GlyLeuMetGluArgProAspTirpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
Db 90 GlyLeuMetGluArgProAspTirpGluThrAlaIleGlnLysProLeuCysSerLeuPro 109
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664 GGGCTCCTAGATCGCCCTGACTGGAGGAAGCTGTGAAGATGCTGTGGGCATCCTCCCC 723
110 AlaGlySerGlyAsnAlaLeuAlaAAserLeuAsnHisTyrAlaGlyTyrGluGlnVal 129
724 TGGGGCTCGGGCAACGGCTGGCGGAGAGTGAACAGCAGCGGGGATTTGAGCGAGCC 783
130 ThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerPro 149
784 CTGGGCTCGACCTGTTGCTCACTGCTCACTGTGCTGTGGCGGGGTGGTGGCCACCCA 843
150 MetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPheSerValLeuSerLeu 169
944 CTGACCTGCTTCCGAGCGCTGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG 903
170 AlaTrpGlyPheLeuAlaAspValAspLeuLeuGluSerAspLysTyrArgLeuGlyGlu 189
904 GCCTGGGGCTTCGTGTCAGATGTGATATCCAGAGCGAGCTTCAGGGCTTGGGAGCT 963
190 MetArgPheThrLeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArg 209
964 GCCCGCTTCACTGGGCGAGGCTGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 1023
210 LeuAlaThrLeuProVal----- 215
1024 CTCCTCTACTCTCCCGCCACTGTGTGAACCTGCTGCGCCACCCCTGCGCCATAGCTGCCT 1083
215 ----- 215
1084 CGTGCCAAAGTCGGAGCTGACCTAACCAGAGCCAGCCCGCCCGCCACTCACCC 1143
215 ----- 215
1144 CTGCATCCTTCTGTGTCTGACCTGCTCTTCCCTGCTGCGCCAGCTGCGCTGCTCTCT 1203
215 ----- 215
1204 GGCTGGCCAGAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1263
215 ----- 215
1264 GACTGGGGTGGGGTGGGATGCTCCGCTGTCCCGGAGCCACTGCTGTCTTCCACTCCT 1323
216 -----GlyArgValGlyPheLeuThrProAlaSer-----ProValValValGln 230
1324 GGCTCTCCCAAGGAGCTCTACACTACCCGCTTCCGAGGGGCCCCGPAATTCGCCCA 1383
231 Gln-----GlyPro 233
1384 TCCTCTGGGCTCCCACTTCCACCCCTGATGCTGCGGGCTAGGGGCTCCACTGCGGCCG 1443
234 ValAspAlaHisLeuValProLeuGluGlnValProSerHisTrpGlnValValPro 253
1444 CCCGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
254 AspGluAspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPhe 273
1501 GAGGGGACTTGTGCTCATGTGGCCATCTGCGCCAGCCACTAGCGGCTGAGCTGGTG 1560
274 AlaAlaProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValAlaGly 293
1561 GCAGCTCGCATGCGCGCTTCGACGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
294 ValSerArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMetGlu 313
1621 ATCTCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
314 TyrGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAsp 333
1681 CTGGGCTGCTCGCAGCTGGGCTAGCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
334 GlyLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGln 353
1741 CCACGGCGGCTGCTCACAGTGGACGGGAGCAGGTGAGTATGGGCGGCTACAGGCACAG 1800

QY 354 ValHisProAsnTyrPheTrpMetValSerGlyCysValGluProProProSerTyrLys 373
Db 1801 ATGCACCTCGCATCGGTACACTGCTACTGCG-----CTCTCTGGTGC--- 1845
QY 374 ProGlnGlnMetProProProGluGluPro 383
Db 1846 -----CCGGGGCGGAGGCC 1860

RESULT 14

US-10-348-052-24
; Sequence 24, Application US/10348052
; Publication No. US20030219782A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Henrik
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
; OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
; FILE REFERENCE: 200116.405
; CURRENT APPLICATION NUMBER: US/10/348.052
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-348-052-24

Alignment Scores:
Pred. No.: 7,578-58 Length: 2629
Score: 550.00 Matches: 146
Percent Similarity: 46.59% Conservative: 66
Best Local Similarity: 32.09% Mismatches: 125
Query Match: 27.30% Indels: 118
DB: 15 Gaps: 14

US-09-784-810C-2 (1-384) x US-10-348-052-24 (1-2629)

QY 12 ProArgProCys-----ArgValLeuValLeuLeuAsnProArgGlyGlyGlyLys 29
Db 784 CCGCGGATTTGGGCAACAGTTGCTCTACTGATCCGAAATCCGTTCCGGGCAA 843
QY 30 AlaLeuGlnLeuPheArgSerHisValGlnProLeuLeuAlaGluAlaGluSerPhe 49
Db 844 GGGCTGAGCTCTTCCAGAAACAGTGGCACCCTTGTGACGGAAGCAGAGTGCATATC 903
QY 50 ThrLeuMetLeuThrGluArgAsnHisAlaArgGluLeuValArgSerGluGlu--- 68
Db 904 GATCTCCAGATCACACACATCCGAGTATGCCAAGGAGTTCGTGCGGACCAAGGAT 963
QY 69 ---LeuGlyArgTrpAspAlaLeuValValMetSerGlyAspGlyLeuMetHisGluVal 87
Db 964 CTGCTGACACCGTATTCGGGCAATTGTGTTGCTTCCGCGGATGTTCTATTCTACGAGTG 1023
QY 88 ValAsnGlyLeuMetGluArgProAspTrpGluThrAlaLeuGlnLys---ProLeuCys 106
Db 1024 CTCATGGGCTAATGAAACGATGATTTGGCGCGGAGCTTCAGGGAGCTACCGTTGGC 1083
QY 107 SerLeuProAlaGlySerGlyAsnAlaLeuAlaLeuAlaLeuSerLeuAsnHisTyrAlaGly--- 125
Db 1084 ATTATACCATGTGTTCCGGGAATGCTCTGGCAAAAGTGTGGCCCATCATTCGAATGAA 1143
QY 126 ---TyrGluGlnValThrAsnGluAspLeuLeuThrAsnCysThrLeuLeuCysArg 144
Db 1144 CCGTACGAAACCGAAGCC-----ATTCTCCAGCCACCTTGAACCTGATGTCGG 1191
QY 145 ProValLeuSerProMetAsnLeuLeuSerLeuHisThrAlaSerGlyLeuArgSerPhe 164
Db 1192 GGCARAAGTACACCCATGATGTGCTCAGAGTGGAGTGGGAGCGGACGACAGCACATT 1251
QY 165 -----SerValLeuSerLeuAlaTrpGlyPheLeuAlaAspValAspLeuGluSer 181

```
b 1252 GTGATGTACTCTCTCGTGGTGGGCTCTGATAGCGGACATCGATATAGAGAGC 1311
Y 182 AsplysTyArgArgLeuGlyGluMetArgPheThrLeuGlyThrPheLeuArgLeuAla 201
b 1312 GAGGATTTAGATCGATTGGAGCCCAAGGTTTACGTGTGGGCCATCAAGCGATTGATC 1371
Y 202 AlaLeuArgThrTyArgGlyArgLeuAlaThrLeuProValGlyArgValGlyPheLys 221
b 1372 GGGCTGCGCAGCTACAAAGCGCGAGTGTCTATCTA---CTGGGCAAG---GGCAAGAAG 1425
Y 222 ThrProAlaSerProVal----- 227
b 1426 GAACCA-----CCAGTGGAAAGCGGCTCGAGAGTTGCTCGAGAATCAACGGCTGCAGGA 1479
Y 228 ValValGlnGlnGlyProValAspAla-----HisLeuValProLeuGluGlu--- 243
b 1480 ATCGCTCATCTCTGCTCTGATGATCGCGGGAATTCATGATCTACCCGAGGAGGAG 1539
Y 243 ----- 243
b 1540 GGGGAGCGGCTTGGATGGAGAACAGTTGCGCGATGCCATATCTTTGGATCGTTCGGTT 1599
Y 243 ----- 243
b 1600 TACGCCAGATGCCAGATGTGGCACTCGGCCATGTCCAGCGAACGCATATTACTCC 1659
Y 243 ----- 243
b 1660 CTGGCGGACCCAGTATCGATCCAAATCGACCGGATGAGCATTAGCCAGCGATCCAG 1719
Y 244 -----GlnVal 245
b 1720 GCAGCAAAATCGGAATTCGCTGAGAGGTCGCAACGGCGCACCATTCACCATACAGATG 1779
Y 246 Pro-----SerHisTrpGlnValValProAspGluAspPheValLeuValLeuAla 262
b 1780 CCATGCTCAGCAGCGATGTTGGATCTCGAGAGATGGTACATTGTGATGGTCCATGCC 1839
Y 263 LeuLeuHisSerHisLeuAlaSerGluMetPheAlaAlaProMetGlyArgCysAlaAla 282
b 1840 GCCTATACCAACCATCTCTCTCGATGTCCTTTTCGGCCCGAATCCCGTCTGGACGAT 1899
Y 283 GlyValMetHisLeuPheTyValArgAlaGlyValSerArgAlaMetLeuLeuArgLeu 302
b 1900 GGCCTCACTACCTGGTATCCGAGAGGCGTTAGTCGCCATCAGCTGTCAATTTC 1959
Y 303 PheLeuAlaMetGluLysGlyArgHisMetGluTyr---GluCysProTyrLeuValTyr 321
b 1960 ATGCTGAACCTAAACGAGGACCCATCTGCCCATCGCGAGGATCGTTTCATCAAGGTG 2019
Y 322 ValProValValAlaPheArgLeuGluProLysAspGlyLysGlyValPheAlaValAsp 341
b 2020 GTGCTTGTGGGCATTCGGCATCGAGCGGAGCAGCTCCGATGGCATCTGTGTGGTGAC 2079
Y 342 GlyGluLeuMetValSerGluAlaValGlnGlnValHisPro 356
b 2080 GCGAGCGGGTGAATATGACCCATTTCAGCGGAGGTATGCCC 2124
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RESULT 15

S-10-348-052-25

Sequence 25, Application US/10348052

Publication No. US20030219782A1

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

TITLE OF INVENTION: Fyrtst, Henrik

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION

OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

FILE REFERENCE: 200116 405

CURRENT APPLICATION NUMBER: US/10/348,052

CURRENT FILING DATE: 2003-01-17

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

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; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-348-052-25
```

Alignment Scores:

Pred. No.:	1-16e-50	Length:	2609
Score:	492.50	Matches:	139
Percent Similarity:	45.15%	Conservative:	61
Best Local Similarity:	31.38%	Mismatches:	131
Query Match:	24.44%	Indels:	113
DB:	15	Gaps:	11

US-09-784-810C-2 (1-384) x US-10-348-052-25 (1-2609)

QY	16	ArgValLeuValLeuLeuAsnProArgGlyGlyLysGlyLysAlaLeuGlnLeuPheArg	35
DB	755	CGAGTGTCTGTCTGTGAATCCAAATCCGGTCCGGTACGCTCGTGGAGTCTTCAAC	814
QY	36	SerHisValGlnProLeuAlaGluAlaGluLeuSerPheThrLeuMetLeuThrGlu	55
DB	815	ATGCAGCTGACCCCGTGTCTCAACGAGCGCGAGGTGCCCTAGACCTGTATGTAAACCAAG	874
QY	56	ArgArgAsnHisAlaArgGluLeuValArgSerGluGluLeuGlyArgTrpAspAlaLeu	75
DB	875	CATTCCAACTTTTGCATCGAGTCTTTGAGCACCAACGCTGCTGGACGCTGTGTGTCGGTG	934
QY	76	ValValMetSerGlyAspGlyLeuMetHisGluValValAsnGlyLeuMetGluArgPro	95
DB	935	GTGGGTGTGCGGAGAGCGGTCTCTCCACGAGATGATCAATGGACTGCTGCAGCGCCAG	994
QY	96	AspTrpGluThrAlaIle---GlnIysProLeuCysSerLeuProAlaGlySerGlyAsn	114
DB	995	GACTGGGCCCATCGTCTGCTCATCTGGCACTGGGAATCATCTCTTGGCGCTCCGGAAT	1054
QY	115	AlaLeuAlaAlaSerLeuAsnHisTyrAlaGlyTyrGluGlnValThrAsnGluAspLeu	134
DB	1055	GGATTTGGCGCGTCCATTTGCCAT-----TGTTACACAAGCAGCATG	1096
QY	135	LeuThrAsnCysThrLeuLeuLeuCysArgProValLeuSerProMetAsnLeuLeuSer	154
DB	1097	CTA---GGAGCTGCTCTACCGTAACTAGTGGACGCACTTACCCTATGAGCGTGGTCCGG	1153
QY	155	LeuHisThrAlaSerGlyLeuArgSer---PheSerValLeuSerLeuAlaTrpGlyPhe	173
DB	1154	GTGCAGCTGCAGAT-----CGCTCCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT	1207
QY	174	IleAlaAspValAspLeuGluSerAspLysTyrArgArgLeuGlyGluMetArgPheThr	193
DB	1208	ATCTCGGACGTGGACATCGAGGCGGCGCATTCGCATGTTGGGCTACCGCGCTTCACC	1267
QY	194	LeuGlyThrPheLeuArgLeuAlaAlaLeuArgThrTyrArgGlyArgLeuAlaThrLeu	213
DB	1268	GTGTGGACCCCTACCGTCTGTGTGAATCTGCGCACCTACACGCGCCGATCAGTATCTT	1327
QY	213	----- 213	
DB	1328	CTGACGGACCATGAGGTGTCTCTCAACCCATAGCGTACCGGTATTGTGCCCGCGAGA	1387
QY	214	-----ProVal 215	
DB	1388	ATGCAGAGACCGGTAGCTGCAACACGCAATCGACATGCTAAATGGGCGCGGCCCATC	1447
QY	216	GlyArgValGlyPheLeuThrProAlaSerProValValGlnGlnGlnGlnGlnGlnGln	235
DB	1448	TATCATTCAGTGC---CGAGTACCTGGCACAGAGTTTTCGCGACGCTGATCTCCCTGGAGAC	1506
QY	236	AlaHis-----LeuValProLeuGlu----- 242	
DB	1507	GTCCATCAATCAGTCTTCCCTCGAGGTGCGACAGCTGGTGTGTGGGGGATCGCGCGC	1566
QY	243	-----GluGlnValPro----- 246	

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Db 1567 CAGCTTTTACTATTCCATATCGGAGAGCATCTACCACAGTCTGGCGGATGAGAGCGAGTT 1626
Qy 246 ----- 246
Db 1627 CGCGGGCTGGCGGCGCCCTCGCTGGAACACCGGACAGCAGAACTACGCTCCGGCAAGCGA 1686
Qy 247 -----Ser-HisTyrGlnValValProAspG1 255
1687 GCTGCCGATCTGAACGAACCGCTGTCGGAGGATCAGGGTTGG---CTGGTGAGGAGGG 1743
Qy 255 uAspPheValLeuValLeuAlaLeuHisSerHisLeuAlaSerGluMetPheAlaAl 275
1744 CGAGTTGCTCATGATGCACGCCGTTTACCAGACCCATCTGGGCATCGACTGTCATTTCG 1803
Qy 275 aProMetGlyArgCysAlaAlaGlyValMetHisLeuPheTyrValArgAlaGlyValSe 295
1804 GCCCAAGGCCAGCTGAACGACGCGCACCATCTACCTGATCCTCATACGCGCGGATCAG 1863
Qy 295 rArgAlaMetLeuLeuArgLeuPheLeuAlaMetGluLysGlyArgHisMet---GluTyr 314
1864 CGCGCGCACCTGCTGAGCTTCTCTACACATGAGCTCGGCACTCACCTGCCGAGTC 1923
Qy 314 rGluCysProTyrLeuValTyrValProValValAlaPheArgLeuGluProLysAspG1 334
1924 GCACGACGACCATGTGAAGGTGCTGCGAGTGCAGTGCAGCATTCGCGCTGGAGCCCTACGCAA 1983
Qy 334 YLysGlyValPheAlaValAspGlyGluLeuMetValSerGluAlaValGlnGlyGlnVa 354
1984 TCACGGCATCATCAGGTCGACGCGGAGCGGCTCGAGTTCGGGCCCCCTCCAGCTGAGGT 2043
Qy 354 LHisPro 356
2044 CCGGCCG 2050
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Search completed: February 27, 2004, 22:34:07
Job time : 423 secs